

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 19, 2002, 22:22:25 ; Search time 2799.87 Seconds  
(without alignments)  
3778.556 Million cell updates/sec

Title: US-09-196-427-2

Perfect score: 489

Sequence: 1 ATGAGATTTCGAACACCA.....TGTTCAACACACTCTTGA 489

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	489	100.0	489	1	PCT-US01-04130A-2
2	489	100.0	489	6	US-08-233-606-4
3	489	100.0	489	9	US-08-504-042A-1
4	489	100.0	489	9	US-08-567-342-1
5	489	100.0	489	15	US-09-134-134-2
6	489	100.0	489	29	US-09-724-841-1
7	489	100.0	489	29	US-09-724-848-2
8	489	100.0	489	29	US-09-743-416-4
9	489	100.0	1202	17	US-09-349-216-9
10	489	100.0	1202	18	US-09-442-384A-569
11	489	100.0	1202	21	US-09-543-679A-2909
12	489	100.0	1202	32	US-09-849-014-1
13	489	100.0	1346	60	US-60-213-360-743
14	489	100.0	1615	56	US-60-172-373-1761
15	489	100.0	1630	71	US-60-324-185-4211
16	489	100.0	17904	21	US-09-543-679A-2912
17	487.8	99.8	1126	29	US-09-758-457-65
18	487.4	99.7	489	18	US-09-437-585-5
19	481	98.4	489	18	US-09-437-585-7
20	465	95.1	489	6	US-08-233-606-1
21	465	95.1	489	15	US-09-134-134-1
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23	465	95.1	489	29	US-09-724-848-1
24	465	95.1	489	29	US-09-743-416-3
25	451.4	92.3	453	14	US-09-016-434-1486
26	405.4	82.9	694	29	US-09-758-457-28
27	400	81.8	409	17	US-09-362-510-44336
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30	380	77.7	643	14	US-09-023-655-9655
31	380	77.7	2165	56	US-60-172-373-15309

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Sequence 1, Appli  
Sequence 572, App  
Sequence 154, App  
Sequence 861, App  
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Sequence 12, Appl  
Sequence 16948, A  
Sequence 13, Appl  
Sequence 1, Appli  
Sequence 2910, Ap

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33 378.4 77.4 1248 21 US-09-543-679A-2908  
34 378.4 77.4 1248 32 US-09-856-748-1  
35 358 73.2 358 16 US-09-221-481-572  
36 358 73.2 358 18 US-09-442-384-154  
37 358 73.2 358 18 US-09-442-385-861  
38 357 73.0 357 18 US-09-442-384-154  
39 351.6 71.9 486 21 US-09-543-679A-2911  
40 345 70.6 345 29 US-09-724-841-12  
41 337 68.9 1244 75 US-09-360-207-16948  
42 325.8 66.6 345 29 US-09-724-841-13  
43 141.6 29.0 14968 1 PCT-US01-04130A-1  
44 141.6 29.0 14968 1 PCT-US01-04130A-111  
45 141.6 29.0 14968 21 US-09-543-679A-2910

ALIGNMENTS

RESULT 1  
PCT-US01-04130A-2  
; Sequence 2, Application PC/TUS0104130A  
; GENERAL INFORMATION:  
; APPLICANT: Genaisance Pharmaceuticals, Inc.  
; APPLICANT: Nandabalan, Krishnan  
; APPLICANT: Stephens, J. Claiborne  
; APPLICANT: Chew, Anne  
; APPLICANT: Anastasio, Allison  
; APPLICANT: Denton, R. Rex  
; TITLE OF INVENTION: DRUG TARGET ISOGENES:  
; FILE REFERENCE: MMH-0048 PCT IL15  
; CURRENT APPLICATION NUMBER: PCT/US01/04130A  
; CURRENT FILING DATE: 2001-02-08  
; PRIOR APPLICATION NUMBER: 60/181,059  
; PRIOR FILING DATE: 2000-02-08  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 489  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US01-04130A-2

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Best Local Similarity 100.0%; Pred. No. 7.7e-110;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 atgagaatttcgaaccacatttgagaagtatttccatccagtgctacttgtgttactt 60

QY 61 CTAACAGTCTATTTCTAACTGAAGCTGGCATTCTTCTCATTTTGGGCTGTTTCACT 120  
DB 61 ctaaacagtcattttctaaactgaagctggcatttcttctcatcttgggctgttctagt 120

QY 121 CGAGGGCTTCTTAAACAGACCCAACTGGGTGAATGTAAGTATTTGAAAAAATT 180  
DB 121 gcagggtcttctaaacagacccaaactgggtgaattgtaagtattgaaaaaatt 180

QY 181 GAAGATCTTATTCATCTATGCATATTGATGCTACTTTATATACGGAAGTGTTCAC 240  
DB 181 gaagatcttattcaatctatgcatactgctacttattatatacggaagtgtgttcac 240

QY 241 CCAGTTCGAAGTAAACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTATTTCATT 300  
DB 241 cccagttcgaagttaaacagcaatgaagtcttctcttggagttacaaagtattttcatt 300

QY 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTAGAAAAATCTGATCATCTAGCAAAAC 360  
DB 301 gagtcggagatgcaagtatttcattgatacacagtagaaaaatctgatcatctcctagcaaac 360

QY 361 AGTTGTGTTCTTAATGGGAATGTACAGATCTGGATCAAGAATGTGAGGAACGTGAG 420  
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DB 421 gaaaaaataataagaatttttgcagagttttgtacattttgtccaaatgttccatcaac 480

QY 481 ACTTCTTGA 489  
DB 481 acttcttga 489

RESULT 2  
US-08-233-606-4  
; Sequence 4, Application US/08233606  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: Epithelium-derived T-cell Factor  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/233,606  
; FILING DATE: 22-APR-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/031,399  
; FILING DATE: 08-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Launer, Charlene  
; REGISTRATION NUMBER: 33,035  
; REFERENCE/DOCKET NUMBER: 2811  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
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Best Local Similarity 100.0%; Pred. No. 7.7e-110;  
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QY	61	CTAAACAGTCATTTCTTAACCTGAAGCTGGCATTCATGCTCTTCATTTGGGCTGGTTTCAGT	120	
DB	61	CTAAACAGTCATTTCTTAACCTGAAGCTGGCATTCATGCTCTTCATTTGGGCTGGTTTCAGT	120	
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DB	181	GAAGATCTTATTCAAATCTATGCATATTTGATGCTACTTTATATACGGAAAGTCATGTTTCACT	240	
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US-08-567-342-1  
; Sequence 1, Application US/08567342  
; GENERAL INFORMATION:  
; APPLICANT: Quinn, LeBris  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Troutt, Anthony B.  
; TITLE OF INVENTION: Muscle-Trophic Factor  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: System 7, Word 5.1a  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/567,342  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Malaska, Stephen L.  
; REGISTRATION NUMBER: 32,655  
; REFERENCE/DOCKET NUMBER: 2833  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 1:

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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
US-08-567-342-1

Query Match          100.0%; Score 489; DB 9; Length 489;
Best Local Similarity 100.0%; Pred. No. 7.7e-110;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACACATTTGAGAGATTTTCCATCCAGTCTACTTGTGTTTACTT 60
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QY 61 CTAACAGTCATTTCTAACTGAAGCTGGCATTCATGCTCTTTTGGGCTGTTTCAGT 120
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QY 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAGAATACTGATCATCTAGCAACAAC 360
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Db 361 AGTTGCTCTTAATGGGAATGTAACAGAACTGGATGCAAGAAATGTGAGGAACCTGGAG 420
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Db 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 480
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Db 481 ACTTCTTGA 489

RESULT 5
US-09-134-134-2
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Paxton, Raymond
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Antagonists of IL-15
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Word for Windows 95, 7.0
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,134
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US/08/392,317
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
US-09-134-134-2

Query Match          100.0%; Score 489; DB 15; Length 489;
Best Local Similarity 100.0%; Pred. No. 7.7e-110;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACACATTTGAGAGATTTTCCATCCAGTCTACTTGTGTTTACTT 60
Db 1 ATGAGAAATTCGAAACACATTTGAGAGATTTTCCATCCAGTCTACTTGTGTTTACTT 60
QY 61 CTAACAGTCATTTCTAACTGAAGCTGGCATTCATGCTCTTTTGGGCTGTTTCAGT 120
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Db 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAGAATACTGATCATCTAGCAACAAC 360
QY 361 AGTTGCTCTTAATGGGAATGTAACAGAACTGGATGCAAGAAATGTGAGGAACCTGGAG 420
Db 361 AGTTGCTCTTAATGGGAATGTAACAGAACTGGATGCAAGAAATGTGAGGAACCTGGAG 420
QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 480
Db 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 480
QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 6
US-09-724-841-1
; Sequence 1, Application US/09724841
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
```





Db	737	gaaaaaataattaagaatttttgcagagttttgtacatttgcataattgtccaaatgttcataaac	796
QY	481	ACTCTCTGA	489
Db	797	actctcttga	805

```

RESULT 10
US-09-442-384A-569
; Sequence 569, Application US/09442384A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey
; TITLE OF INVENTION: Hematology/Immunology Array
; FILE REFERENCE: CLON-006CIP15
; CURRENT APPLICATION NUMBER: US/09/442.384A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 830
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 569
; LENGTH: 1202
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-442-384A-569

```

Query Match	100.0%;	Score 489;	DB 18;	Length 1202;
Best Local Similarity	100.0%;	Pred. No. 9.9e-110;		
Matches 489;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	ATGAGAAATTTCGAAACCAACATTTGAGAAGTATTTCATCCAGGCTACCTGTGGTTTCACTT	60
Db	317	atgagaatttcgaaacacacatttgaagaagtatttcocatccagtgctaacttggtttcaact	376
QY	61	CTAAACAGTCAATTTCTAACTGAAGCTGCAATTCATGCTCTCATTTTGGCGTGTTCAGT	120
Db	377	ctaaacagtcattttctaaactgaagctggcaattcagtctcatttggcgctgttccagt	436
QY	121	GCAGGGTTCCTTAAACACAGAAGCCAACCTGGGTGAATGTAATAGTGCATTTGAAAAAAT	180
Db	437	gcaggggttctctaaacacagaagccaaactgggtgaatgtaataagtgatttggaaaaaatt	496
QY	181	GAAGATCTTTATTCANCTATTCGCATATTGATGCTACTTTATATACGGAAAGTGATGTTCA	240
Db	497	gaagatctttattccaattctatgcataattgatgctaactttatatacggaaagtgatgttca	556
QY	241	CCGAGTTGCAAGATTACAGCAATGAAGTGGCTTTCTCTTGAGTTACAAGTTATTTCACTT	300
Db	557	ccgagttgcgaagttaacagcaatgaagtgctttctctctcttgaggttacaagttatttcaact	616
QY	301	GAGTCCGGAGATCGAAGTATTCATGATACAGTAGAAAACTGATCATCTCGCAACAACAC	360
Db	617	gagtcctggagatcaagtatctcatgatacagtagaaaactctgatactcatcctagcaaaaac	676
QY	361	AGTTTGTCTTCTAATGGGAATGTAACAGAAATCTGGATGCAAGAAATGTGAGAAACGTGAG	420
Db	677	agtttgtctctaatg99gaatgttaaagaaatctcgagatctcgaaagaaagt99gaacctcgag	736
QY	421	GAAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC	480
Db	737	gaaaaaataataaagaatttttgcagagtttttgatacatgtgtccaaatgttcatcaac	796
QY	481	ACTTCTTGA	489
Db	797	acttcttga	805

RESULT 11  
US-09-543-679A-2909  
; Sequence 2909, Application US/09543679A  
; GENERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.  
 TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE  
 COMPOSITIONS, KIT & METHOD FOR TREATMENT  
 OF AIRWAY DISORDERS ASSOCIATED WITH  
 BRONCHOCONSTRICTION, LUNG INFLAMMATION,  
 NUMBER OF SEQUENCES: 3111  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
 STREET: 7 Clarke Drive  
 CITY: Cranbury  
 STATE: NJ  
 COUNTRY: USA  
 ZIP: 08512  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: CD-R  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: N/A  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/543,679A  
 FILING DATE: 13-Apr-2000  
 CLASSIFICATION: UNKNOWN  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/127,958  
 FILING DATE: 1998-08-03  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Amzel, Viviana  
 REGISTRATION NUMBER: 30,930  
 REFERENCE/DOCKET NUMBER: EPI-0067191b  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 609-409-3035  
 TELEFAX: 413-254-9245  
 TELEX: <UNKNOWN>  
 INFORMATION FOR SEQ ID NO: 2909:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1202 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2909:  
 US-09-543-679A-2909

```
Query Match      100.0%; Score 489; DB 21; Length 1202;
Best Local Similarity 100.0%; Pred. No. 9.9e-110;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	1	ATGAGAAATTCGAAACCAACATTTGAGAGATATTTCATCCAGTGTACTGTGTTTCACT	60
Db	317	ATGAGAAATTCGAAACCAACATTTGAGAGATATTTCATCCAGTGTACTGTGTTTCACT	376
Qy	61	CTAAACAGTCATTTCTTAACCTGAAGCTGGCATTCATGCTTCATTTTGGCGTGTTCAGT	120
Db	377	CTAAACAGTCATTTCTTAACCTGAAGCTGGCATTCATGCTTCATTTTGGCGTGTTCAGT	436
Qy	121	GCAGGGCTTCCTAAAACAGAACCAACTGGGTGAATGTATAATAGTGATTTGAAAAAATT	180
Db	437	GCAGGGCTTCCTAAAACAGAACCAACTGGGTGAATGTATAATAGTGATTTGAAAAAATT	496
Qy	181	GAGATCTTATTCAATCTATGCATATTGATGCTACTTTATATACGAAAGTGCATGTTAC	240
Db	497	GAGATCTTATTCAATCTATGCATATTGATGCTACTTTATATACGAAAGTGCATGTTAC	556
Qy	241	CCCAGTTGCAAAATAACAGCAATGAAGTGGTTCTCTCTGGAGTTACAAGTTATTTCACTT	300
Db	557	CCCAGTTGCAAAATAACAGCAATGAAGTGGTTCTCTCTGGAGTTACAAGTTATTTCACTT	616
Qy	301	GAGTCCGGAGATCAAGTATTCATGATACAGTAGAAAATCTGATCATCTCTAGCAACAC	360
Db	617	GAGTCCGGAGATCAAGTATTCATGATACAGTAGAAAATCTGATCATCTCTAGCAACAC	676
Qy	361	AGTTTGTCTCTTAATGGGAATGTAAACAGAAATCTGGATGCAAAAGAAATGTGAGGAATGGAG	420

Db 677 AGTTGTTCTTCTAATGGGATCTAACAGATCTGGATGCAAGAATGTGAGGAAGTGGAG 736  
QY 421 GAAAAAATATTAAAGAAATTTTTCAGAGATTTGTACATATTGTCCAAATGTTTCATCAAC 480  
|||||  
Db 737 GAAAAAATATTAAAGAAATTTTTCAGAGATTTGTACATATTGTCCAAATGTTTCATCAAC 796  
QY 481 ACTTCTTGA 489  
|||||  
Db 797 ACTTCTTGA 805

## RESULT 12

US-09-849-014-1

; Sequence 1, Application US/09849014  
; GENERAL INFORMATION:  
; APPLICANT: BEN GURION UNIVERSITY OF THE NEGEV  
; APPLICANT: MOR - RESEARCH APPLICATIONS LTD.  
; TITLE OF INVENTION: ANTISENSE OLIGOMER  
; FILE REFERENCE: A34255 PCT USA-A  
; CURRENT APPLICATION NUMBER: US/09/849,014  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: IL126919  
; PRIOR FILING DATE: 1998-11-05  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1202  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-09-849-014-1

Query Match 100.0%; Score 489; DB 32; Length 1202;  
Best Local Similarity 100.0%; Pred. No. 9.9e-110;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAACACCATTTGAGAGATATTTCCATCCAGTCTACTTGTGTTTACTT 60  
Db 317 atggaatttcgaaccacatttgagaagatttccatccagtgctacttgttttaactt 376  
QY 61 CTAACAGCTCATTTTCTAACTGAAGCTGGCATTCATGTCTTCATTTGGGTGTTTCAGT 120  
Db 377 ctaaacagctcattttctaactgaagctggcattcatgtcttctcattttgggtgtttcagt 436  
QY 121 GCAGGGCTTCTAAACAGAGCCAACTGGGTGAATGTAATGATGATTTGAAAAAATTT 180  
Db 437 gcagggtctctaacaacagaccactgggtgaatgtaataagtgatttgaaaaaaatt 496  
QY 181 GAAGATCTTATTCAATCTATCATATGCTACTTCTTATATACGGAAGTGAATGTTTCAAC 240  
Db 497 gaagatcttattcaatctcatgcatattgatgctacttctatatatacggaagtgatgttcac 556  
QY 241 CCCAGTTGCAAGTAACAGCAATGAAGTGTCTTCTTGGAGTTACAAGTTATTTCACTT 300  
Db 557 cccagttgcaagtaaacagcaatgaagtgcttctctcttgagttacaagttatttcaactt 616  
QY 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTACAGTAAGAAATCTGATCATCTAGCAAAACAC 360  
Db 617 gagtcggagatgcaagtatttcattcatgatacagtagaataatctgatcctcctagcaaacac 676  
QY 361 AGTTTGCTTCTTAATGGAATGTAACGAATCTGGATGCAAGATGTGAGGAAGTGGAG 420  
Db 677 agtttgccttctaattggaatgtaacgaatctggtgcaagaagtgtgaggaactggag 736  
QY 421 GAAAAAATATTAAAGAAATTTTTCAGAGATTTGTACATATTGTCCAAATGTTTCATCAAC 480  
Db 737 gaaaaaataataagaatttttcagagattttgtacatattgtccaaatgttcatcaac 796  
QY 481 ACTTCTTGA 489  
|||||  
Db 797 acttcttga 805

## RESULT 13

US-60-213-360-743  
; Sequence 743, Application US/60213360  
; GENERAL INFORMATION:  
; APPLICANT: MORRIS, MacDonald  
; APPLICANT: Lai, Preeti  
; APPLICANT: Diep, Dinh  
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Poly  
; TITLE OF INVENTION: Identified Thereby  
; FILE REFERENCE: CX-0014 P  
; CURRENT APPLICATION NUMBER: US/60/213,360  
; CURRENT FILING DATE: 2000-06-21  
; NUMBER OF SEQ ID NOS: 8347  
; SOFTWARE: PERL Program  
; SEQ ID NO 743  
; LENGTH: 1346  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No: 1082250.1  
; NAME/KEY: unsure  
; LOCATION: 1248  
; OTHER INFORMATION: a, t, c, g, or other

US-60-213-360-743

Query Match 100.0%; Score 489; DB 60; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 1e-109;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAACACCATTTGAGAGATATTTCCATCCAGTCTACTTGTGTTTACTT 60  
Db 136 atggaatttcgaaccacatttgagaagatttccatccagtgctacttgttttaactt 195  
QY 61 CTAACAGCTCATTTTCTAACTGAAGCTGGCATTCATGTCTTCATTTGGGTGTTTCAGT 120  
Db 196 ctaaacagctcattttctaactgaagctggcattcatgtcttctcattttgggtgtttcagt 255  
QY 121 GCAGGGCTTCTAAACAGAGCCAACTGGGTGAATGTAATGATGATTTGAAAAAATTT 180  
Db 256 gcagggtctctaacaacagaccactgggtgaatgtaataagtgatttgaaaaaaatt 315  
QY 181 GAAGATCTTATTCAATCTATCATATGCTACTTCTTATATACGGAAGTGAATGTTTCAAC 240  
Db 316 gaagatcttattcaatctcatgcatattgatgctacttctatatatacggaagtgatgttcac 375  
QY 241 CCCAGTTGCAAGTAACAGCAATGAAGTGTCTTCTTGGAGTTACAAGTTATTTCACTT 300  
Db 376 cccagttgcaagtaaacagcaatgaagtgcttctctcttgagttacaagttatttcaactt 435  
QY 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTACAGTAAGAAATCTGATCATCTAGCAAAACAC 360  
Db 436 gagtcggagatgcaagtatttcattcatgatacagtagaataatctgatcctcctagcaaacac 495  
QY 361 AGTTTGCTTCTTAATGGAATGTAACGAATCTGGATGCAAGATGTGAGGAAGTGGAG 420  
Db 496 agtttgccttctaattggaatgtaacgaatctggtgcaagaagtgtgaggaactggag 555  
QY 421 GAAAAAATATTAAAGAAATTTTTCAGAGATTTGTACATATTGTCCAAATGTTTCATCAAC 480  
Db 556 gaaaaaataataagaatttttcagagattttgtacatattgtccaaatgttcatcaac 615  
QY 481 ACTTCTTGA 489  
|||||  
Db 616 acttcttga 624

## RESULT 14

US-60-172-373-1761  
; Sequence 1761, Application US/60172373  
; GENERAL INFORMATION:



```

; APPLICANT: Morris, MacDonald
; APPLICANT: Lai, Preeti
; APPLICANT: Disp, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymorp
; FILE REFERENCE: GX-0006 P
; CURRENT APPLICATION NUMBER: US/60/172,373
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 1761
; LENGTH: 1615
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 348901.2
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 104, 1517
; OTHER INFORMATION: a, t, c, g, or other
US-60-172-373-1761

```

Query Match	100.0%;	Score 489;	DB 56;	Length 1615;
Best Local Similarity	100.0%;	Pred. NO. 1.1e-109;		
Matches 489;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGAGAAATTCGAACACACATTTGAGAGAGTATTTCCATCCAGTGCCTACTTGTGTTACTT	60	
DB	405	atgagaatttcgaaccacacatttgagaagctattccatccagtcactgttgaact	464	
QY	61	CTAACAGTCAATTTCTAACTGAAGCTGGCATTCATGTCTTCATTTGGGCTGTTTCAGT	120	
DB	465	ctaaacagtcattttcttaactgaagctggcattcatgtcttcattttgggctgttcaagt	524	
QY	121	GCAGGGTTCTCTAAACAGAGCCACATGGGTGAATGTAAAGTGAATTCGAAAAAATT	180	
DB	525	gcagggttctcctaaacagagcccaactgggtgaatgtaataagtgattgaaaaaatt	584	
QY	181	GAAGATCTTATTCAATCTATGCATATTGCTCTACTTTTATATACGGGAAGTGATGTTCAAC	240	
DB	585	gaagattttattcaattcattgcatttgactactttatatacgggaagtgatgttcaac	644	
QY	241	CCCAGTTGCAAGTAAACAGCAATGAAGTGCCTTCTCTGGAGTACAAAGTATTTCACCT	300	
DB	645	cccagttgcgaagtaacagcaatgaagtgccttctcttggagttacaagttatttcaact	704	
QY	301	GAGTCCGAGATGCAAGTATTTCATGTACAGTAGAANAATCTGATCATCCTTAGCAACAAC	360	
DB	705	gagtcgggagatgcaagtattcatgacagtagaanaatctgatcactagcaaacac	764	
QY	361	AGTTTGTCTCTAATGGGAATGTAAACGAATCTGGATGCAAGGAATGTAGGAAGTGGAG	420	
DB	765	agttctgtcttctaattgggaa tgaacagaa cctggatgcaagaagtgcgaggaactggag	824	
QY	421	GAAAAAATATTAAAGAAATTTTTCGACAGTTTTGTACATATATGTGCCAATGTTCATCAAC	480	
DB	825	gaaaaaatattaagaatttttgcagagtttgcacattatgtcccaaatgttcatcaac	884	
QY	481	ACTTCTTGA	489	
DB	885	acttcttga	893	

RESULT 15  
US-60-324-185-42H1  
; Sequence 4211, Application US/60324185  
; GENERAL INFORMATION:  
; APPLICANT: Morris MacDonald  
; APPLICANT: Lal, Preeti  
; APPLICANT: Diep, Dinh  
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING

```

; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO 4211
; LENGTH: 1630
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1082250.1
; NAME/KEY: unsure
; LOCATION: 1532
; OTHER INFORMATION: a, t, c, g, or other
US-60-324-185-4211

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```

Query Match      100.0%; Score 489; DB 71; Length 1630;
Best Local Similarity 100.0%; Pred. No. 1.1e-109;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	1	ATGAGAAATTTGCGAAACACACATTTGAGAAGTATTTCCTCATCCAGTCCTACTTGTGTTTACTTT	60
Db	420	atgagaatttcgaaacacacatttgagaagtatttccatccagtgctacttggtttactt	479
QY	61	CTAACAAGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCATTTTGGGCTGCTTTTCAGT	120
Db	480	ctaaacagtcattttctaaactgaagctggcattcatgtcttctattttgggctgtttcagt	539
QY	121	GCAGGGCTTCCTAAACACAGAAGCCAACCTGGCTGGATCTAATAGTCATTTGAAAAAATT	180
Db	540	gcagggtctctctaaacacagaagcccaactgggtgaagtgaataagtgatttggaaaaaatt	599
QY	181	GAGATCTTATTTCAATCTATGTCATATTGATGCTACTTTATATACGGAAAGTGATGTTTCAC	240
Db	600	gaagatcttattccaatctatgcataattgatgcactttatatacggaagtgatgttcac	659
QY	241	CCAGTTGCGAAGTAACAGCAATGAAGTGCTTTCTCTTGGAGTTACAAGTTATTTCACTT	300
Db	660	cccagttgcgaagttaacagcgaatgaagtgcttctctcttgaggttacaagttatttcactt	719
QY	301	GAGTCCGGAGATCGAAGTATTCATGATACAGTAGTAAGAACTGTAATCTGATCATCTAGACAAAC	360
Db	720	gagtcggggagatcgaagtatctatgatcacagtgaataatctgcatcctcagcaaacac	779
QY	361	AGTTTGTCTTCTAATGGGAATGTAAACGAATCTGGATGCAAAAGATCTGAGGAACCTGGAG	420
Db	780	agtttgtctctctaatgggaatgttaacagaatctcgatgcaaaagaatgtgaaggaaactggag	839
QY	421	GAAAAAATAATTAAGAAGATTTTTCGACAGGTTTTGTACATATTCTCCAAATGTTTCATCAAC	480
Db	840	gaaaaaataattaaagaattttgcagagtttgcagatttgcacatttgcceaaatgttccatcaac	899
QY	481	ACTTCTTGA	489
Db	900	acttcttga	908

Search completed: September 20, 2002, 00:12:06  
Job time: 6581 sec





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Db 241 ccagttgcaagtaacagcaatgaagtgtcttctcttgaggtacaaagtatttcaactt 300
QY 301 GAGTCGGAGATCAAGTATTCAATGATACAGTAGAGAAATCTGATCATCTTAGCAACAAC 360
Db 301 ggtccggagatgcaagtattcatgatagacagttagaatactgatcatcctagcaacaac 360
QY 361 AGTTTGTCTTCTTAATGGGAATGTAAACAGAACTGGGATGCAAGAAATGTGAGGAAG 420
Db 361 agttgtcttctaatgggaatgtaacagaatctggatgcaagaatgtgaggaactggag 420
QY 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTGATATATGTCACAAATGTTCAATCAAC 480
Db 421 gaaaaaataattaaagaatttttgcagagtttttgcagagttttgtacatatgtccaaatgttcatcaac 480
QY 481 ACTTCTTGA 489
Db 481 acttcttga 489

RESULT 2
US-09-953-323A-3
; Sequence 3, Application US/09953323A
; GENERAL INFORMATION:
; APPLICANT: Strom, Terry B.
; APPLICANT: Li, Xian Chang
; TITLE OF INVENTION: MODULATION OF IL-2 AND IL-15 MEDIATED T CELL RESPONSES
; FILE REFERENCE: 01948-057001
; CURRENT APPLICATION NUMBER: US/09/953,323A
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US 60/232,251
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(486)
US-09-953-323A-3

Query Match 100.0%; Score 489; DB 5; Length 489;
Best Local Similarity 100.0%; Pred. No. 8.3e-108;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAATTTGAAACACCATTTGAGAGTATTTCATCCAGTGTCTACTTGTGTTTACTT 60
Db 1 atgagaatttcgaaccacatttgagaagtatttcattccagtgctacttggtttactt 60
QY 61 CTAAACAGTCATTTCTAACTGAAGCTGGCATTCATGTCTTCAATTTGGGCTGTTTCACT 120
Db 61 ctaaacagtcattttctaactgaagctggcattcgtcttcatcttgggctgtttcagt 120
QY 121 GCAGGGCTTCTAAACAGAGCCAACTGGGTGAATGTAATGAAGTATTAAGTATTTCAAT 180
Db 121 gcagggtctctaaacagagccaaactgggtgaatgtaataagtgatttgaaaaaatt 180
QY 181 GAAGATCTTATTCATCTATGATGCTACTTATATACGAAAGTATGATGCTTCACT 240
Db 181 gaagatcttattcaatctatgcatattgatgctactttatatacgaagtgatgttcaac 240
QY 241 CCCAGTTGCAAGTAACAGCAATGAAGTGTCTTCTTGGAGTTACAAGTATTATTTCACTT 300
Db 241 cccagttgcaagtaaacagcaatgaagtgtcttcttggagttacaagttatttcaactt 300
QY 301 CCCAGTTGCAAGTAACAGCAATGAAGTGTCTTCTTGGAGTTACAAGTATTATTTCACTT 360
Db 301 cccagttgcaagtaaacagcaatgaagtgtcttcttggagttacaagttatttcaactt 360
QY 361 GAGTCGGAGATGCAAGTATTCAATGATACAGTAGAGAAATCTGATCATCTTAGCAACAAC 420
Db 361 ggtccggagatgcaagtattcatgatagacagttagaatactgatcatcctagcaacaac 420
QY 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTGATATATGTCACAAATGTTCAATCAAC 480
Db 421 gaaaaaataattaaagaatttttgcagagtttttgcagagttttgtacatatgtccaaatgttcatcaac 480
QY 481 ACTTCTTGA 489
Db 481 acttcttga 489

RESULT 3
US-09-053-375B-567
; Sequence 567, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 567
; LENGTH: 1202
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-053-375B-567

Query Match 100.0%; Score 489; DB 5; Length 1202;
Best Local Similarity 100.0%; Pred. No. 9.9e-108;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAATTTGCAACACCATTTGAGAGTATTTCATCCAGTGTCTACTTGTGTTTACTT 60
Db 317 atgagaatttcgaaccacatttgagaagtatttcattccagtgctacttggtttactt 376
QY 61 CTAAACAGTCATTTCTAACTGAAGCTGGCATTCATGTCTTCAATTTGGGCTGTTTCACT 120
Db 377 ctaaacagtcattttctaactgaagctggcattcgtcttcatcttgggctgtttcagt 436
QY 121 GCAGGGCTTCTAAACAGAGCCAACTGGGTGAATGTAATGAAGTATTAAGTATTTCAAT 180
Db 437 gcagggtctctaaacagagccaaactgggtgaatgtaataagtgatttgaaaaaatt 496
QY 181 GAAGATCTTATTCATCTATGATGCTACTTATATACGAAAGTATGATGCTTCACT 240
Db 497 gaagatcttattcaatctatgcatattgatgctactttatatacgaagtgatgttcaac 556
QY 241 CCCAGTTGCAAGTAACAGCAATGAAGTGTCTTCTTGGAGTTACAAGTATTATTTCACTT 300
Db 557 cccagttgcaagtaaacagcaatgaagtgtcttcttggagttacaagttatttcaactt 616
QY 301 GAGTCGGAGATGCAAGTATTCAATGATACAGTAGAGAAATCTGATCATCTTAGCAACAAC 360
Db 617 ggtccggagatgcaagtattcatgatagacagttagaatactgatcatcctagcaacaac 676
QY 361 AGTTTGTCTTCTTAATGGGAATGTAAACAGAACTGGGATGCAAGAAATGTCAGAGTCGAG 420
Db 677 agtttgtcttctaatgggaatgtaacagaatctggatgcaagaatgtgaggaactggag 736
QY 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTGATATATGTCACAAATGTTCAATCAAC 480
Db 737 gaaaaaataattaaagaatttttgcagagtttttgcagagttttgtacatatgtccaaatgttcatcaac 796
QY 481 ACTTCTTGA 489
Db 797 acttcttga 805

RESULT 4
```

```
|||||
Db 361 agtttgtcttctctcaagggaatgaacagaatctggtgcaagaatgtgaggaactggag 420
QY 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTGATATATGTCACAAATGTTCAATCAAC 480
Db 421 gaaaaaataattaaagaatttttgcagagtttttgcagagttttgtacatatgtccaaatgttcatcaac 480
QY 481 ACTTCTTGA 489
Db 481 acttcttga 489

RESULT 3
US-09-053-375B-567
; Sequence 567, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 567
; LENGTH: 1202
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-053-375B-567

Query Match 100.0%; Score 489; DB 5; Length 1202;
Best Local Similarity 100.0%; Pred. No. 9.9e-108;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAATTTGCAACACCATTTGAGAGTATTTCATCCAGTGTCTACTTGTGTTTACTT 60
Db 317 atgagaatttcgaaccacatttgagaagtatttcattccagtgctacttggtttactt 376
QY 61 CTAAACAGTCATTTCTAACTGAAGCTGGCATTCATGTCTTCAATTTGGGCTGTTTCACT 120
Db 377 ctaaacagtcattttctaactgaagctggcattcgtcttcatcttgggctgtttcagt 436
QY 121 GCAGGGCTTCTAAACAGAGCCAACTGGGTGAATGTAATGAAGTATTAAGTATTTCAAT 180
Db 437 gcagggtctctaaacagagccaaactgggtgaatgtaataagtgatttgaaaaaatt 496
QY 181 GAAGATCTTATTCATCTATGATGCTACTTATATACGAAAGTATGATGCTTCACT 240
Db 497 gaagatcttattcaatctatgcatattgatgctactttatatacgaagtgatgttcaac 556
QY 241 CCCAGTTGCAAGTAACAGCAATGAAGTGTCTTCTTGGAGTTACAAGTATTATTTCACTT 300
Db 557 cccagttgcaagtaaacagcaatgaagtgtcttcttggagttacaagttatttcaactt 616
QY 301 GAGTCGGAGATGCAAGTATTCAATGATACAGTAGAGAAATCTGATCATCTTAGCAACAAC 360
Db 617 ggtccggagatgcaagtattcatgatagacagttagaatactgatcatcctagcaacaac 676
QY 361 AGTTTGTCTTCTTAATGGGAATGTAAACAGAACTGGGATGCAAGAAATGTCAGAGTCGAG 420
Db 677 agtttgtcttctctcaagggaatgtaacagaatctggatgcaagaatgtgaggaactggag 736
QY 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTGATATATGTCACAAATGTTCAATCAAC 480
Db 737 gaaaaaataattaaagaatttttgcagagtttttgcagagttttgtacatatgtccaaatgttcatcaac 796
QY 481 ACTTCTTGA 489
Db 797 acttcttga 805

RESULT 4
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US-09-442-384B-569  
; Sequence 569, Application US/09442384B  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; APPLICANT: Lukashev, Matvey  
; TITLE OF INVENTION: Hematology/Immunology Array  
; FILE REFERENCE: CLON-006CIP15  
; CURRENT APPLICATION NUMBER: US/09/442,384B  
; PRIOR FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 09/053,375  
; PRIOR FILING DATE: 1998-03-31  
; NUMBER OF SEQ ID NOS: 830  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 569  
; LENGTH: 1202  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-442-384B-569

Query Match 100.0%; Score 489; DB 5; Length 1202;  
Best Local Similarity 100.0%; Pred. No. 9.9e-108;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ATGAGAAATTCGAAACACACATTTGAGAAGTATTTCCATCCAGTCTACTTGTTTACTT 60  
Db 317 atgagaaattcgaaacacacatttgagaagtatttccatccagtgctacttggtttactt 376  
  
QY 61 CTAAACAGCTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTTGGGCTCTTTTCAGT 120  
Db 377 ctaaacagctcatTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTTGGGCTCTTTTCAGT 436  
  
QY 121 GCAGGGCTTCTTAAACAGAACCCAACTGGGTGAATGTATTAAGTGAATTTGAAAAAAAT 180  
Db 437 gcagggttcttTAAACAGAACCCAACTGGGTGAATGTATTAAGTGAATTTGAAAAAAAT 496  
  
QY 181 GAGATCTTATCAATCTATGATATTTGATGCTACTTTATATACGGAAGTGAATGTTTCAAC 240  
Db 497 gagatcttTATCAATCTATGATATTTGATGCTACTTTATATACGGAAGTGAATGTTTCAAC 556  
  
QY 241 CCCAGTTGCAAAAGTAAACAGCAATGGAAGTCTTCTTGGAGTTACAAAGTTATTTTCACTT 300  
Db 557 cccagttgCAAAAGTAAACAGCAATGGAAGTCTTCTTGGAGTTACAAAGTTATTTTCACTT 616  
  
QY 301 GAGTCCGGAGATCAAGTATTTATGATACAGTAAAGTGAATCTGATCATCTCTAGCAAAACAAC 360  
Db 617 gagtccggagATCAAGTATTTATGATACAGTAAAGTGAATCTGATCATCTCTAGCAAAACAAC 676  
  
QY 361 AGTTTGTCTTCTAATGGGAATGTAACAGAAATCTGGATGCAAGAAATGTGAGGAACCTGGAG 420  
Db 677 agtttgtctTCTAATGGGAATGTAACAGAAATCTGGATGCAAGAAATGTGAGGAACCTGGAG 736  
  
QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 480  
Db 737 gaaaaaATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 796  
  
QY 481 ACTTCTTGA 489  
Db 797 acttcttga 805

RESULT 5  
US-10-219-925-65/c  
; Sequence 65, Application US/10219925  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PM042CJN  
; CURRENT APPLICATION NUMBER: US/10/219,925  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 09/758,457  
; PRIOR FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: 60/179,065

; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 806  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 65  
; LENGTH: 1126  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-219-925-65

Query Match 99.8%; Score 487.8; DB 6; Length 1126;  
Best Local Similarity 99.4%; Pred. No. 1.9e-107;  
Matches 486; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ATGAGAAATTCGAAACACACATTTGAGAAGTATTTCCATCCAGTCTACTTGTTTACTT 60  
Db 826 ATGAGAAATTCGAAACACACATTTGAGAAGTATTTCCATCCAGTCTACTTGTTTACTT 767  
  
QY 61 CTAAACAGCTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTTCAGT 120  
Db 766 CTAAACAGCTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTTCAGT 707  
  
QY 121 GCAGGGCTTCTTAAACAGAACCCAACTGGGTGAATGTATTAAGTGAATTTGAAAAAAAT 180  
Db 706 GCAGGGCTTCTTAAACAGAACCCAACTGGGTGAATGTATTAAGTGAATTTGAAAAAAAT 647  
  
QY 181 GAGATCTTATCAATCTATGATATTTGATGCTACTTTATATACGGAAGTGAATGTTTCAAC 240  
Db 646 GAGATCTTATCAATCTATGATATTTGATGCTACTTTATATACGGAAGTGAATGTTTCAAC 587  
  
QY 241 CCCAGTTGCAAAAGTAAACAGCAATGGAAGTCTTCTTGGAGTTACAAAGTTATTTTCACTT 300  
Db 586 CCCAGTTGCAAAAGTAAACAGCAATGGAAGTCTTCTTGGAGTTACAAAGTTATTTTCACTT 527  
  
QY 301 GAGTCCGGAGATCAAGTATTTATGATACAGTAAAGTGAATCTGATCATCTCTAGCAAAACAAC 360  
Db 526 GAGTCCGGAGATCAAGTATTTATGATACAGTAAAGTGAATCTGATCATCTCTAGCAAAACAAC 467  
  
QY 361 AGTTTGTCTTCTAATGGGAATGTAACAGAAATCTGGATGCAAGAAATGTGAGGAACCTGGAG 420  
Db 466 AGTTTGTCTTCTAATGGGAATGTAACAGAAATCTGGATGCAAGAAATGTGAGGAACCTGGAG 407  
  
QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 480  
Db 406 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 347  
  
QY 481 ACTTCTTGA 489  
Db 346 acttcttga 338

RESULT 6  
US-09-855-313A-1  
; Sequence 1, Application US/09855313A  
; GENERAL INFORMATION:  
; APPLICANT: Strom, Terry B.  
; APPLICANT: Maslinski, Wlodzimierz  
; APPLICANT: Zheng, Xin Xiao  
; APPLICANT: Kim, Yon Su  
; APPLICANT: Lacraz, Sylvie Ferrari  
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ACHIEVING IMMUNE SUPPRESSION  
; FILE REFERENCE: 01948-056001  
; CURRENT APPLICATION NUMBER: US/09/855,313A  
; CURRENT FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: US 60/203,801  
; PRIOR FILING DATE: 2000-05-12  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 489  
; TYPE: DNA

```

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(486)
US-09-855-313A-1

```

Query Match 98.7%; Score 482.6; DB 5; Length 489;  
Best Local Similarity 99.2%; Pred. NO. 2.8e-106;  
Matches 485; Conservative 0; Mismatches 4; Indels 0

Qy	1	ATGAGAAATTTTCGAAACACACAAATTTTGAGAAAGTATTTTCCATCCAGTGCATCTTGTTGTTTACATT	60
Db	1	atgagaaatttcgaaacacaattttgagaagtatttccatccatcagtgctactgtgtttactt	60
Qy	61	CTAAACAGTCATATTTCTAACTGAAGCTGGCATTCATGCTTTCATTTTGGCTGTTTTCAGT	120
Db	61	ctaaacagtcattttctaaactgaagctggcattcatgtcttcaatttggctggtttccagt	120
Qy	121	GCAGGGTTCCTTAACACAGAACCCAACTGGGTGAATGTGTAATAGTGATTTTGAAAAAAATTT	180
Db	121	gcagggcttctctaaacacagagccaaactgggtgaattgaataagtgtatttgaaaaaaatt	180
Qy	181	GAAGATCTTATTCAAATCTATGTCATATTTGATGCTTACATTTATATACGGAAAGTCATGTTTCAC	240
Db	181	gaagatcttatttcaattctatgcataattgatgtcactttatatcaggaaagtgatggttcaac	240
Qy	241	CCCAGTTGCAAAATTAACAGCAATGAAGTGCTTTCTCTTGAGTTTACAAGTTATTTTCACTTT	300
Db	241	cccagttgcaagatgaacagcaatgaaagtgtcttctcttgggttacaagtatttttcaactt	300
Qy	301	GAGTCGGAGATCCAAGTATTCATGATACAGTAGAAATCTGATCATCTCCTACGAACACAC	360
Db	301	gagtcggagatgcagtgatctcatgatacagtagaaaaactgatcatcctgcagaaacac	360
Qy	361	AGTTTGTCTTCTAATGGGAATTAACAGAAATCTGGATGCAAGAAGATGTGAGGAACCTGGAG	420
Db	361	agtttgtcttctaatgggaatgtaacagaaactcggatgcagaaagatcgtgaggaaactggag	420
Qy	421	GAAGAAAATTAAGAAATTTTTCAGAGCTTTTGACATATTTGTCCAAATGTTTCATCCAC	480
Db	421	gaagaaaatttaagaatttttggcagagtttctgtacataattgtcgacatggttcatcaac	480
Qy	481	ACTCTTTGA	489
Db	481	actctttga	489

```

RESULT      7
US-09-953-323A-1
; sequence 1, Application US/09953323A
; GENERAL INFORMATION:
; APPLICANT: Strom, Terry B.
; APPLICANT: Li, Xian Chang
; TITLE OF INVENTION: MODULATION OF IL-2 AND IL-15 MEDIATED T CELL RESPONSES
; FILE REFERENCE: 01948-057001
; CURRENT APPLICATION NUMBER: US/09/953,323A
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US 60/232,251
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(486)
US-09-953-323A-1

```

Query Match 98.7%; Score 482.6; DB 5; Length 489;

Best Local Similarity		99.28;	Pred. No. 2.8e-106;	Matches 485; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
Qy	1	ATGAGAATTTTCGAACACACATTTGAGAAAGTATTTCCATCCAGTCTACTCTGTGTTTACTT	60		
Db	1	atgagaatttcgaacacacacatttgagaagtattccatccagtctactgtgttactt	60		
Qy	61	CTAAACAGTCAATTTCTTAACGTGAAGCGGCGAATCATGCTTTCAATTTGGGCGTGTTCAGT	120		
Db	61	ctaaacagtcattttctaactgaagctggcattcatgtcttcattttgggctgttcagt	120		
Qy	121	GCAGGGCTTCCTAAACACAGAACCAACTGGCTGAATGTAACTGATTTTCAGAAAATTT	180		
Db	121	gcagggtcttcctaaacacagaagccactggcgtaagttaa caagtcgacttgaaaaaatt	180		
Qy	181	GAAGATCTTATTCATCTATGACATATTGATGCTACTTTATATAGCGAAAGTGATGTTTCAAC	240		
Db	181	gaagattcttattcaactctatgcatatgatgctactttatatacggaaagtgatgttcac	240		
Qy	241	CCCAGTTCGCAAGTAAACAGCAATCAAGTGCCTTTCTCTTCCTGGAGTTTACAAGTTATTTCAC	300		
Db	241	cccgatgcaagtaacagcaaatgaagtcgtcttctctgtggagttcacagttatttccatt	300		
Qy	301	GAGTCCGGAGATCGAAGTATTCATGATACAGTACAGAAATCTGATCCTAGCAAAACAAC	360		
Db	301	gagtcggagatgcaagtattcatgatacagtagaataatctgatcctcctagcaaaacaac	360		
Qy	361	AGTTTGCTTCTAATGGGAATGTAAACAGATCTCGATGTCGAAAGATGTGAGGAACCTGGAG	420		
Db	361	agtttgtcttctaattgggaatgtaacagaaatctctggatgcaaaagaaatgtgaggaactggag	420		
Qy	421	GAATAAATATTAAGAAATTTTTCACAGAGTTTCTGACATATTGTCCTCAAAATGTCATCAAC	480		
Db	421	gaataaataataaagaattttttggacagttttgacattatgtcgacatggttcatcaac	480		
Qy	481	ACTTCTTGA	489		
Db	481	acttcttga	489		

```

RESULT      8
US-10-2119-925-28
; Sequence 28, Application US/10219925
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM042C1N
; CURRENT APPLICATION NUMBER: US/10/219,925
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 09/758,457
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 806
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (651)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (681)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-2119-925-28

```

Query Match 82.9%; Score 405.4; DB 6; Length 694;

```

Best Local Similarity 97.4%; Pred. No. 9.9e-88;
Matches 443; Conservative 0; Mismatches 8; Indels 4; Gaps 3;

Qy 1 ATGAGATTTTCGAACACACATTTGAGAGTATTTTCCATCCAGTCTACTTCTGTTTACTT 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 241 atgagatttcgaaacacatttgagaagtatttccatccagtcacttgigttaactt 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 CTAACAGTCATTTTCTAACGTAAGCTGGCATTGTCATGCTTTCATTTTGGGCTGTTTCAGT 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 301 ctaacagtcattttcttaactgaagctggcattcatgtcttcattttgggctgttcagt 360
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 121 GCAGGGTTCTCTAAACAGAGCCAACTGGGTGAATGTATTAAGTGTATTTGAAAAAATT 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 361 gcaagggttctcctaaacagagccaaactggcgaaatgtaacaagtgatttgaaaaaaatt 420
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 181 GAAGATTTTATTCATCTATGTCATATTTATGCTACTTATATACGCGAAAGTGATGTTCCAC 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 421 gaagattttattcaactatgtcatatgatgtactttatatcaggaaagtgatgttcac 480
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 241 CCCAGTTGCAAGTAACAGCAATGAAGTGCTTCTCTGGAGTTACAAGTTATTTTCACTT 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 481 cccagttgcaaaagcaacagcaaatgaagtgcttctctctgtggagttacaagttatttcactt 540
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 301 GAGTCCGAGATGCAAGTATTTCATGATACAGTACAGAAATCTGATCATCTAGCAAAACAAC 360
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 541 gagtcgagatgcaagtatttcagatcacagtagaagaatctgatcatcctagcaaacacac 599
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 361 AGTTTGCTTCTTAATGGGAATGTAACAGATCTTGGATGCAAGAAATGTGAGGAACCTGG- 418
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 600 agtttgccttctaattgggaatgtaacagaactctggatgccagaatgtgangaactggg 659
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 419 -AGCAAAAAATATTAAGGATTTTTCAGAGTTT 452
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 660 aggaaaaaattttaagaanttttgcagagttt 694
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9
US-09-442-366A-1102
; Sequence 1102, Application US/09442366A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Likashev, Matvey E.
; TITLE OF INVENTION: Human Array
; FILE REFERENCE: CLON-006CIP13
; CURRENT APPLICATION NUMBER: US/09/442,366A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 2216
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 1102
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic gene fragment
US-09-442-366A-1102

```

	Query Match	73.2%	Score 358;	DB 5;	Length 358;
	Best Local Similarity	100.0%;	Pred. No. 2e-76;		
	Matches 358;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	22	TTGAGAAAGTATTTCATCCAGTCGTACTGTGTTGTACTTCTAAACAGTCATTTTCTTAAC	81		
Db	1	tTgagagTatttcattccatccagTgctactTgtttactTctaaacagTcattttctaact	60		
Qy	82	GAAAGCTGCATTCATGCTTTCATTTTGGCTGTGTTTCAGTCGAGGGCTCTCTAAACAGAA	141		
Db	61	gaagctggcattcagTcttcaattttgggctgtttcagTgcagggcttcttaaacagaa	120		
Qy	142	GCCAACTGGGTGAATGTAATAAGTGATTGAAAAAAAATTGAAGATCTTATTCAATCTATG	201		

Db	121	gccaaactgggtgaatgtaataagtgatttgaataaatggaagaatcttattcaatcatgtg	180
Qy	202	CATATTGATGGTACTTTTATATACGGAAAGTGATGTTCACCCCAAGTTGCCAAAGTAACAGCA	261
Dd	181	cataattgatgcactttatatacgaaaagtgaattcccccaggttgcaaaagtaaacagca	240
Qy	262	ATGAAGTGCCTTCTCTGGAGTTTACAAGTTTATTTCTACTTGAGTCCCGAGATGCAAGTATT	321
Dd	241	atgaagtgtcttctctctgttgaggttcacagtttatctcattgagtcctcgagatgcaagtatt	300
Qy	322	CATCATACAGTAGAAAAATCTGCATCCTAGCAAACAACAGTTTGTCTCTAATGGGA	379
Dd	301	catgatcacgttagaaaaatctgacctctagcaacaacacagttctgtctctaagggga	358
 RESULT 10 US-09-442-384B-154			
; Sequence 154, Application US/09442384B			
; GENERAL INFORMATION:			
; APPLICANT: Chenchlik, Alex			
; APPLICANT: Lukashiev, Matvey			
; TITLE OF INVENTION: Hematology/Immunology Array			
; FILE REFERENCE: CLON-006CIP15			
; CURRENT APPLICATION NUMBER: US/09/442,384B			
; CURRENT FILING DATE: 1999-11-17			
; PRIOR APPLICATION NUMBER: 09/053,375			
; PRIOR FILING DATE: 1998-03-31			
; NUMBER OF SEQ ID NOS: 830			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 154			
; LENGTH: 357			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Nucleic Acid Probe.			
US-09-442-384B-154			

Query Match	73.0%;	Score 357;	DB 5;	Length 357;
Best Local Similarity	100.0%;	Pred. No. 3.5e-76;		
Matches 357;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps
QY	22	TTGAGAAGTATTTCCATCCAGTGCTACTCTGTGTTTACTTCTAAACAGTCATTTTCTTAAC	81	
Db	1	ttgagaagttattccattccagtgctactctgctttactcttcaaacagtcattttctcaact	60	
QY	82	GAACTGGCATTCATGTCATTTTGGGTGTTTCAGTGCAGGGTCTCTAAACACGAA	141	
Db	61	gaagctggcatcattgctctcattttgggctgtttcagtcgagggtctctaaaacagaa	120	
QY	142	GCCAACTGGGTGAATGTAATAAGTGATTTCGAAAATAATTAAGACATCTTATTCATCTATC	201	
Db	121	gccaaactgggtggaatgtaataagtgatttgaaaaaaatggaagatcttattccaattcta	180	
QY	202	CATATTGATGCTACTTTTATATACGGAAGTGATGTTTCACCCCAGTTGCAAAAGTAACAGCA	261	
Db	181	catattgatgctactctttatatacggaagtgatgtttcaccccgatgcaaaagtaacagca	240	
QY	262	ATGAAGTGCCTTCTCTGTGGAGTTACAAAGTTATTTCACTTCAGTCCGAGATGCAAGTATT	321	
Db	241	atgaagtgccttctctctctcttgagggttacaagttatttctacttgagtcggagagtcgaagt	300	
QY	322	CATGATACAGTAGAANAATCGATCATCTAGCAACAACAGTTTGTTGTTCTTAATGGG	378	
Db	301	catgatacagtagaaaatctgatactcctagcaacaacagttgttcttctaagtgg	357	
RESULT	11			
US-09-053-375B-1144				
; Sequence 1144, Application US/09053375B				
; GENERAL INFORMATION:				
; APPLICANT: Chenchik, Alex				
; APPLICANT: Bibilashvili, Robert				

```

: TITLE OF INVENTION: Nucleic Acid Arrays
: FILE REFERENCE: CLON-006
: CURRENT APPLICATION NUMBER: US/09/053,375B
: CURRENT FILING DATE: 1998-08-31
: NUMBER OF SEQ ID NOS: 1543
: SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ ID NO 1144
: LENGTH: 1250
: TYPE: DNA
: ORGANISM: Mus musculus
US-09-053-375B-1144

```

Query Match	68.98;	Score	337;	DB	5;	Length	1250;
Best Local Similarity	80.6%;	Pred. No.	2.8e-71;				
Matches	394;	Conservative	0;	Mismatches	95;	Indels	0;
0;							
Qy	1	ATGAGAATTCGAAACACACATTTGAGAGATATTTCCTCCAGTCTACTTGTGTTACTTT	60				
Db	466	atgaaaatttgaacacatatatgaggaatacacaccatctogtctactgtgttctct	525				
Qy	61	CTAAACAGTCATTTCCTTAACCTGAAGCTGGCATTCATGCTTCATTTTGGGCTGTTTCAGT	120				
Db	526	ctaaacagtcactttttaactgagctggcacttcattcttcatttgggctgtgtcagt	585				
Qy	121	GCAGGGTTCCTAAAACAGAACCCCACTGGGTGAATGTAATTAAGTGATTTTGAAGAAAAATT	180				
Db	586	gtaggctccctaaaacagagggcccaactggatagatatgaagatatgacctggagaaatt	645				
Qy	181	GAAGATCTTATTCAATCTATGTCATATTGATGCTACTTATATACGGAAAGTGATGTTCAAC	240				
Db	646	gaaagccttactcaatattcatattgacaccactttatacactgcagtgactttcat	705				
Qy	241	CCCAAGTTCGAAAAGTAACAGCAATGAAGTGCTTCTCTTGGAGTTTACAAGTTATTTTCAGTT	300				
Db	706	cccaagttgaaaagttaactgcaatgaactgtcttctctctggaattgcagggttattttacat	765				
Qy	301	GAGTCGGAGATGCAAGTATTATGATACAGTAAAGAAATCTGATCATCTTAGCAAAACAC	360				
Db	766	gagtcagtgtaacatgactctttaatgaaacagtaagaaacgtgctcactctgcaaacagc	825				
Qy	361	AGTTGTCTTCTTAATGGGAATGTAACAGAACTCTGGATGCAAGAAATGTGAGGAAGTCTGGAG	420				
Db	826	acctgtctctcaacagaataatgacagaactctggctgcaaggaaatgtgaggagctggag	885				
Qy	421	GAAGAAATAATTAAAGAAATTTTGCACAGATTTTGTACATATTGTCCAAATGTTTCATCAAC	480				
Db	886	gagaaaaccttcacagagtttttgcaaaagctttatacgcgattgtccaaatgtttcatcaac	945				
Qy	481	ACTCTTTGA	489				
Db	946	acgtcctga	954				

```

RESULT      12
US-10-191-803-72
; Sequence 72, Application US/10191803
; GENERAL INFORMATION:
; APPLICANT: MENDRICK, Donna
; APPLICANT: PORTER, Mark
; APPLICANT: JOHNSON, Kory
; APPLICANT: HIGGS, Brandon
; APPLICANT: CASTLE, Arthur
; APPLICANT: ELASHOFF, Michael
; TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5090US
; CURRENT APPLICATION NUMBER: US/10/191.803
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,819
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305,623
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/369,351
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; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US 60/377,611
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 1140
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 1313
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: GenBank Accession No. NM_013129
US-10-191-803-72

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Query Match	67.9%;	Score 332.2;	DB 6;	Length 1313;
Best Local Similarity	80.0%;	Pred. No. 4e-70;		
Matches 391;	Conservative 0;	Mismatches 98;	Indels 0;	Gaps
Qy 1	ATGAGAAATTCGAAACACATTTTGAGAACTATTCCATCCAGTGCCTACTTGTTTCACTT	60		
Db				
546	atgaaaatcttgaaacccatataatgaggaatacatccatctgtactactcgtgttccct	605		
Qy 61	CTAAACAGTCATTTTCTAACTGAAGTGGCATTCATGTCTTCATTTGGGGTGGTTTCAGT	120		
Db				
606	ctcaacagtcactcttaactgagctgagctgccatgctcttcattttbggctgtgtcagt	665		
Qy 121	GCAGGGTTCCTTAAACAGAGCCAACTGGGTGAATGTAATTAAGTGATTTGAAAAAATTT	180		
Db				
666	gtaggctctccctaaacagagggccaaactggatagatgaagatacagactggagaaaaatt	725		
Qy 181	GAAGATCTTATCAACTATGCTATATTGATGTACTCTTATATACGGAAAGTGATGTTCCAC	240		
Db				
726	gaaagctctattccatttattcattatgatactactatcactacagcagactgttccat	785		
Qy 241	CCCAGTTGCAAAAGTAACAGCAATGAAGTGCTTCTCTGGAGTTACAAAGTTTATTTCACTT	300		
Db				
786	cccagttgcaagttactgccaatgaactgctttctccggaaattacaggttatatttgcac	845		
Qy 301	GAGTCGGGAGATGCAAGTATTCATGATACAGTAGAAAATCTGTATCATCCTTAGCAAAACAC	360		
Db				
846	gagtcagtaaacatgactcttaatgaaacagtaagaaacgtgctctactcttgcgaacagc	905		
Qy 361	AGTTTGTCTCTAATGGGAATCTAACAGAACTGATGCAAGATGTCGAGAACTGGAG	420		
Db				
906	acctctgtctcttaacaaagaatgtaatatagctgtggtcgaaggaatgtcgaggactggag	965		
Qy 421	GAAGAAAAATTTAAAGAAATTTTTCAGAGAGTTTGTACATAATTGCCAAATGTTCATCAAC	480		
Db				
966	gagaaacactcacggagtttttgcagagttttatacatattgtccaaatgttccatcaac	1025		
Qy 481	ACTTCTTGA	489		
Db				
1026	acgtcctga	1034		

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RESULT 13
US-09-454-226A-527
; Sequence 527, Application US/09454226A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashhev, Matvey
; TITLE OF INVENTION: Rat Array
; FILE REFERENCE: CLON-006CIP12
; CURRENT APPLICATION NUMBER: US/09/454,226A
; CURRENT FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 1186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 527
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized gene fragmen

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US-09-454-226A-527

Query Match	32.3%;	Score 157.8;	DB 5;	Length 285;
Best Local Similarity	78.4%;	Pred. No. 2e-28;		
Matches 189;	Conservative 0;	Mismatches 52;	Indels 0;	Gaps 0;
Qy 249	CAAAAGTACACGAATGAAGTGCCTTTCTCTTGGAGGTTACAAGTTATTTTCACTTGGAGTCGGG	308		
Db 1	caaggtaactgcaatgaactgcttctctcctggaattacaggtatttttgcagagatacag	60		
Qy 309	AGATGCGAAGTATTTCATGATACAGTAGAAGAAATCTGATCATCTCTAGCAACACACAGTTTGTCTC	368		
Db 61	ttaacatgactctttaatgaaacagtaagaaacgtctctcactttgaaacagcactctgtc	120		
Qy 369	TTCTAATGGGAATGTAACAGAGATCTGGATGCAAGAAATGTGAGGAACCTGGAGGAAAAAAA	428		
Db 121	tcttaacaaagaatgtaataagagtctggctgcaaggaaatgtgaggagctggaggagagaaa	180		
Qy 429	TATTAAAGAAATTTTGCAGAGTTTTGTACATATTTGCCAAATGTTTCATCAACACTCTCTTG	488		
Db 181	cttcacaggagcttttgcagagcttttatcatactgtcccaaatgttccacacagctctgt	240		
Qy 489	A 489			
Db 241	a 241			

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RESULT 14
US-10-216-086-422
; Sequence 422, Application US/10216086
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith
; TITLE OF INVENTION: Novel Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-57
; CURRENT APPLICATION NUMBER: US/10/216,086
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/419,553
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 422
; LENGTH: 181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: mining entry:13176
US-10-216-086-422

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[illegible]

RESULT 15  
US-10-106-698-2528  
; Sequence 2528, Application US/10106698  
; GENERAL INFORMATION:

```

1  APPLICANT: Ruben et al.
2  TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
3  FILE REFERENCE: PA003P1
4  CURRENT APPLICATION NUMBER: US/10/106,698
5  CURRENT FILING DATE: 2002-03-27
6  PRIOR APPLICATION NUMBER: PCT/US00/26524
7  PRIOR FILING DATE: 2000-09-28
8  PRIOR APPLICATION NUMBER: US 60/157,137
9  PRIOR FILING DATE: 1999-09-29
10 PRIOR APPLICATION NUMBER: US 60/163,280
11 PRIOR FILING DATE: 1999-11-03
12 NUMBER OF SEQ ID NOS: 8564
13 SOFTWARE: PatentIn Ver. 3.0
14 SEQ ID NO 2528
15 LENGTH: 565
16 TYPE: DNA
17 ORGANISM: Homo sapiens
18 FEATURE:
19 NAME/KEY: misc_feature
20 LOCATION: (4)..(4)
21 OTHER INFORMATION: n equals a,t,g, or c
22 NAME/KEY: misc_feature
23 LOCATION: (45)..(45)
24 OTHER INFORMATION: n equals a,t,g, or c
25 NAME/KEY: misc_feature
26 LOCATION: (125)..(125)
27 OTHER INFORMATION: n equals a,t,g, or c
28 NAME/KEY: misc_feature
29 LOCATION: (149)..(149)
30 OTHER INFORMATION: n equals a,t,g, or c
31 NAME/KEY: misc_feature
32 LOCATION: (212)..(212)
33 OTHER INFORMATION: n equals a,t,g, or c
34 NAME/KEY: misc_feature
35 LOCATION: (216)..(216)
36 OTHER INFORMATION: n equals a,t,g, or c
37 NAME/KEY: misc_feature
38 LOCATION: (260)..(260)
39 OTHER INFORMATION: n equals a,t,g, or c
40 NAME/KEY: misc_feature
41 LOCATION: (294)..(294)
42 OTHER INFORMATION: n equals a,t,g, or c
43 NAME/KEY: misc_feature
44 LOCATION: (298)..(298)
45 OTHER INFORMATION: n equals a,t,g, or c
46 NAME/KEY: misc_feature
47 LOCATION: (305)..(305)
48 OTHER INFORMATION: n equals a,t,g, or c
49 NAME/KEY: misc_feature
50 LOCATION: (312)..(312)
51 OTHER INFORMATION: n equals a,t,g, or c
52 NAME/KEY: misc_feature
53 LOCATION: (462)..(462)
54 OTHER INFORMATION: n equals a,t,g, or c
55 NAME/KEY: misc_feature
56 LOCATION: (495)..(495)
57 OTHER INFORMATION: n equals a,t,g, or c
58 NAME/KEY: misc_feature
59 LOCATION: (497)..(497)
60 OTHER INFORMATION: n equals a,t,g, or c
61 NAME/KEY: misc_feature
62 LOCATION: (542)..(542)
63 OTHER INFORMATION: n equals a,t,g, or c
64 NAME/KEY: misc_feature
65 LOCATION: (547)..(547)
66 OTHER INFORMATION: n equals a,t,g, or c
67 NAME/KEY: misc_feature
68 LOCATION: (552)..(552)
69 OTHER INFORMATION: n equals a,t,g, or c
70 US-10-106-698-2528

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Query Match 21.0%; Score 102.6; DB 7; Length 565;

Best Local Similarity 83.0%; Pred. No. 3.8e-15;  
Matches 220; Conservative 0; Mismatches 32; Indels 13; Gaps 9;

Qy	1	ATGAGAAATTTGAAACCCACATTT--GAGAAGTATTTCCAT--CCAGTGTCTACTTTGTGTTTA	57
Db	301	atganaatttcnaaacaccacattttgaaaaaattatttccatccccagtgctacttggttta	360
Qy	58	CTTCTAAACAGTCATTTTCTAACT--GAAGCTGGCATT-CATGCTCTCA-TTTTGGGCTG	113
Db	361	cttcttaacaatcatttctaaactgaaagctggcattccatgtcttcatttttgggctg	420
Qy	114	TTTCAGTGCA--GGGCTTCCTAAACACAGAACCCAACTGGGTGAATG-TAATAAGTCATTT	170
Db	421	tttcaatgcaagggttcctcctaaaaaaccacaaactggtnaatgttatttaagtgtatt	480
Qy	171	GAAAAAATT-GAAGATCTTATTAATCATGTCATATTGATGCTACTTTATATAC--GGA	227
Db	481	gaaaaaaatttggaananatttccatctatgccttttgatgctactttattatccggaa	540
Qy	228	AAGTGATCTTCACCCCACTTGCAAA	252
Db	541	anttaanttcnccccattttccaa	565

Search completed: September 20, 2002, 00:17:37  
Job time: 5302 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 19, 2002, 20:25:50 ; Search time 1845.14 Seconds  
(without alignments)  
5545.962 Million cell updates/sec

Title: US-09-196-427-2

Perfect score: 489

Sequence: 1 ATGAGATTTTGGAAACCACA.....TGTTTCATCACACTTCTTGA 489

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*

1: gb.ba:\*

2: gb.htg:\*

3: gb.in:\*

4: gb.om:\*

5: gb.ov:\*

6: gb.pat:\*

7: gb.ph:\*

8: gb.pl:\*

9: gb.pr:\*

10: gb.ro:\*

11: gb.sts:\*

12: gb.sy:\*

13: gb.un:\*

14: gb.vi:\*

15: em.ba:\*

16: em.fun:\*

17: em.hum:\*

18: em.in:\*

19: em.mu:\*

20: em.om:\*

21: em.or:\*

22: em.ov:\*

23: em.pat:\*

24: em.ph:\*

25: em.pl:\*

26: em.ro:\*

27: em.sts:\*

28: em.un:\*

29: em.vi:\*

30: em.htg.hum:\*

31: em.htg\_inv:\*

32: em.htg\_other:\*

33: em.htgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	489	100.0	489	US-09-196-427-2	US-09-196-427-2

1	489	100.0	489	6	AR004268	AR004268 Sequence
2	489	100.0	489	6	AR024349	AR024349 Sequence
3	489	100.0	489	6	AR070281	AR070281 Sequence
4	489	100.0	489	6	AR085740	AR085740 Sequence
5	489	100.0	489	6	AR122046	AR122046 Sequence
6	489	100.0	489	6	AR122868	AR122868 Sequence
7	489	100.0	489	6	AR125105	AR125105 Sequence
8	489	100.0	489	6	AX006786	AX006786 Sequence
9	489	100.0	489	6	AX320244	AX320244 Sequence
10	489	100.0	489	6	I25783	I25783 Sequence 4
11	489	100.0	489	6	I28849	I28849 Sequence 1
12	489	100.0	489	6	I62692	I62692 Sequence 1
13	489	100.0	489	6	I79219	I79219 Sequence 1
14	489	100.0	489	6	AR103280	AR103280 Sequence
15	489	100.0	489	6	AX024715	AX024715 Sequence
16	489	100.0	489	6	AX301227	AX301227 Sequence
17	489	100.0	489	6	HSU14407	HSU14407 Human Inter
18	487.4	99.7	489	6	AR094649	AR094649 Sequence
19	487.4	99.7	489	6	BD008811	BD008811 Antagonis
20	482.6	98.7	489	6	AX320242	AX320242 Sequence
21	481	98.4	489	6	AR094650	AR094650 Sequence
22	481	98.4	489	6	BD008812	BD008812 Antagonis
23	466.6	95.4	492	9	AB000555	AB000555 Macaca fa
24	466.6	95.4	559	9	MMU19843	MMU19843 Macaca m
25	465	95.1	489	6	AR004267	AR004267 Sequence
26	465	95.1	489	6	AR024348	AR024348 Sequence
27	465	95.1	489	6	AR070282	AR070282 Sequence
28	465	95.1	489	6	AR085741	AR085741 Sequence
29	465	95.1	489	6	AR122045	AR122045 Sequence
30	465	95.1	489	6	AR122867	AR122867 Sequence
31	465	95.1	489	6	AR125104	AR125104 Sequence
32	465	95.1	489	6	AX006785	AX006785 Sequence
33	465	95.1	489	6	I25782	I25782 Sequence 1
34	465	95.1	489	6	I28850	I28850 Sequence 4
35	465	95.1	489	6	I79220	I79220 Sequence 4
36	465	95.1	1275	9	CAU03099	CAU03099 Cercopithec
37	451.4	92.3	453	9	HSIL15MR	HSIL15MR H.sapiens m
38	394.6	80.7	489	4	BTU42433	BTU42433 Bos taurus
39	386.6	79.1	489	4	AFI08148	AFI08148 Felis cat
40	386.6	79.1	489	4	SSU58142	SSU58142 Sus scrofa
41	380	77.7	643	9	HSIL15MR1	HSIL15MR1 H.sapiens m
42	380	77.7	643	9	HSIL15MR2	HSIL15MR2 H.sapiens m
43	378.6	77.4	489	4	AFI49700	AFI49700 Ovis arie
44	378.4	77.4	1248	6	AR087004	AR087004 Sequence
45	378.4	77.4	1248	9	AF031167	AF031167 Homo sapi

ALIGNMENTS

RESULT	1	AR004268	489 bp	DNA	linear	PAT 04-DEC-1998
LOCUS	AR004268	Sequence	4	from patent US 5747024.		
DEFINITION	AR004268	Sequence	4	from patent US 5747024.		
ACCESSION	AR004268	Sequence	4	from patent US 5747024.		
VERSION	AR004268.1	GI:3965147				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1	(bases 1 to 489)				
AUTHORS	Grabstein,K.H. and Widmer,M.B.					
TITLE	Vaccine adjuvant comprising interleukin-15					
JOURNAL	Patent: US 5747024-A 4 05-MAY-1998;					
FEATURES	Location/Qualifiers					
source	1..489					
BASE COUNT	159 a	79 c	95 g	156 t		
ORIGIN	/organism="unknown"					

Query Match 100.0%; Score 489; DB 6; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.2e-92;

QY	1	ATGAGAATTTTCGAAACACACATTTGAGAAGTATTTCCATCCAGTGCTACTGTGTTTACTT	60
Db	1	ATGAGAATTTTCGAAACACACATTTGAGAAGTATTTCCATCCAGTGCTACTGTGTTTACTT	60
QY	61	CTAAACAGTGCATTTTCTAACTGAAGCTGGCANTTCATGCTTCTATTTTGGGCTGTTTCAGT	120
Db	61	CTAAACAGTGCATTTTCTAACTGAAGCTGGCATTCTCATTTTGGGCTGTTTCAGT	120
QY	121	GCAGGGCTTCTTAAACAGAGCCAACTGGGTGAATGTAATAGTGAATTTGAAAAAATT	180
Db	121	GCAGGGCTTCTTAAACAGAGCCAACTGGGTGAATGTAATAGTGAATTTGAAAAAATT	180
QY	181	GAAGATCTTATTCATCTATGTCATATTTGATGCTACTTTATACGGGAAGTGATGTTTCA	240
Db	181	GAAGATCTTATTCATCTATGTCATATTTGATGCTACTTTATACGGGAAGTGATGTTTCA	240
QY	241	CCCAGTTGCAAGTAAACAGCAATGAAGTGTCTTCTTTGGAGTTACAGTTATTTCAC	300
Db	241	CCCAGTTGCAAGTAAACAGCAATGAAGTGTCTTCTTTGGAGTTACAGTTATTTCAC	300
QY	301	GAGTCCGGAGATCGAAGTATTCATGATACAGTAGAAGTCTGATCATCTAGCAAAAC	360
Db	301	GAGTCCGGAGATCGAAGTATTCATGATACAGTAGAAGTCTGATCATCTAGCAAAAC	360
QY	361	AGTTTGTCTTCTAATGGGAATTAACAGAATCTGGATGCAAGAAATGTGAGGAAC	420
Db	361	AGTTTGTCTTCTAATGGGAATTAACAGAATCTGGATGCAAGAAATGTGAGGAAC	420
QY	421	GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC	480
Db	421	GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC	480
QY	481	ACTTCTTGA	489
Db	481	ACTTCTTGA	489

RESULT	2
AR024349	
LOCUS	AR024349
DEFINITION	Sequence 2 from patent US 5795966.
ACCESSION	AR024349
VERSION	AR024349.1 GI:3977643
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown. Unclassified.
REFERENCE	1 (bases 1 to 489)
AUTHORS	Grabstein,K.H., Pettit,D.K. and Paxton,R.J..
TITLE	Antagonists of interleukin-15
JOURNAL	Patent: US 5795966-A 2 18-AUG-1998;
FEATURES	Location/Qualifiers 1..489
source	/organism=""unknown"
BASE COUNT	159 a 79 c 95 g
ORIGIN	156 t

	Query Match	100.0%;	Score 489;	DB 6;	Length 489;
	Best Local Similarity	100.0%;	Pred. No. 1.2e-92;		
	Matches 489;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATCAGAAATTCGAAACCAATTTGAGAAGTATTTCCATCCAGTGCCTACTTGTCTTTACTT	60		
Db	1	ATGAGAATTCGAAACCAATTTGAGAAGTATTTCCATCCAGTGCCTACTTGTCTTTACTT	60		
QY	61	CTAAACAGTCATTTTCTTAAGTGAAGCTGGCATTCATGCTCTTCATTTGGGCTGTTTCAGT	120		
Db	61	CTAAACAGTCATTTTCTTAAGTGAAGCTGGCATTCATGCTCTTCATTTGGGCTGTTTCAGT	120		
QY	121	GCAGGGCTTCCTAAAACAGAAGCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAAATT	180		

[illegible]

QY 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAGAGAAATCTGATCATCTAGCAAAAC 360  
|||||  
Db 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAGAGAAATCTGATCATCTAGCAAAAC 360  
|||||  
QY 361 AGTTTCTCTTCTTAATGGGAATGTAACAGAAATCTGGATGCAAGAAATGTGAGGAATGGAG 420  
|||||  
Db 361 AGTTTCTCTTCTTAATGGGAATGTAACAGAAATCTGGATGCAAGAAATGTGAGGAATGGAG 420  
|||||  
QY 421 GAAAAAATATTAAAGAAATTTTGGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480  
|||||  
Db 421 GAAAAAATATTAAAGAAATTTTGGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480  
|||||  
QY 481 ACTTCTTGA 489  
|||||  
Db 481 ACTTCTTGA 489  
|||||

RESULT 4  
AR085740  
LOCUS AR085740 489 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 1 from patent US 5985262.  
ACCESSION AR085740  
VERSION AR085740.1 GI:10012506  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknwn.  
REFERENCE 1 (bases 1 to 489)  
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
TITLE Method of treatment with epithelium derived T-cell factor  
JOURNAL Patent: US 5985262-A 1 16-NOV-1999;  
FEATURES Location/Qualifiers  
source  
i. .489  
/organism="unknown"  
BASE COUNT 159 a 79 c 95 g 156 t  
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.2e-92;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACCAATTTGAGAAGTATTTCCATCCAGTCTACTTGTGTTTACTT 60  
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Db 1 ATGAGAAATTCGAAACCAATTTGAGAAGTATTTCCATCCAGTCTACTTGTGTTTACTT 60  
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QY 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTGGGCTGTTTCAGT 120  
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Db 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTGGGCTGTTTCAGT 120  
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QY 121 GCAGGCTTCTTAAACAGAGCCAACTGGTGAATGTAATAAGTGAATTTGAAAAAAT 180  
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Db 121 GCAGGCTTCTTAAACAGAGCCAACTGGTGAATGTAATAAGTGAATTTGAAAAAAT 180  
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QY 181 GAAGATCTTATTCATCTATGATATGATGCTACTTATATACGGAAGTGAATTTTCACT 240  
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Db 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAGAGAAATCTGATCATCTAGCAAAAC 360  
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QY 481 ACTTCTTGA 489  
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Db 481 ACTTCTTGA 489  
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RESULT 5  
AR122046  
LOCUS AR122046 489 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 2 from patent US 6165466.  
ACCESSION AR122046  
VERSION AR122046.1 GI:14106363  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknwn.  
REFERENCE 1 (bases 1 to 489)  
AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.  
TITLE Antagonists of interleukin-15  
JOURNAL Patent: US 6165466-A 2 26-DEC-2000;  
FEATURES Location/Qualifiers  
source  
i. .489  
/organism="unknown"  
BASE COUNT 159 a 79 c 95 g 156 t  
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.2e-92;  
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QY 481 ACTTCTTGA 489  
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Db 481 ACTTCTTGA 489  
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RESULT 6  
AR122868  
LOCUS AR122868 489 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 2 from patent US 6168783.  
ACCESSION AR122868



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Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 CTAACAGTCATTTCTAACTCAAGCTGGCATTCATGCTTCTCATTTTGGGCTGTTTCAGT 120
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Db 181 GAAGATCTTATCAATCTATGATATGATGCTATTTATATACGGAAGTGTGTTTCAAC 240
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QY 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTTCAACAAC 480
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QY 481 ACTTCTTGA 489
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RESULT 9
AX320244
LOCUS AX320244 489 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 3 from Patent WO0187330.
ACCESSION AX320244
VERSION AX320244.1 GI:17901652
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (sites)
REFERENCE
AUTHORS Strom, T.B. and Maslinski, W.
TITLE Compositions and methods for achieving immune suppression
JOURNAL Patent: WO 0187330-A 3 22-NOV-2001;
BETH Israel Deaconess Medical Center, Inc. (US)
FEATURES
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1..489
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BASE COUNT 159 a 79 c 95 g 156 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 489; DB 6; Length 489;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Best Local Similarity 100.0%; Pred. No. 1.2e-92;
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QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 10
LOCUS I25783 489 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 4 from patent US 5552303.
ACCESSION I25783
VERSION I25783.1 GI:1605653
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 489)
AUTHORS Grabstein, K., Anderson, D., Eisenman, J., Fung, V. and Rauch, C.
TITLE DNA encoding epithelium-derived T-cell factor
JOURNAL Patent: US 5552303-A 4 03-SEP-1996;
FEATURES
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/organism="unknown"
BASE COUNT 159 a 79 c 95 g 156 t
ORIGIN

Query Match
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Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ATGAGATTTTGAAGCCACATTTGAGAGTATTTCCATCCAGTGTCTACTTGTGTTACTT 60
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QY 481 ACTTCTTGA 489  
Db 481 ACTTCTTGA 489  
RESULT 11  
LOCUS I28849 489 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 1 from patent US 5574138.  
ACCESSION I28849  
VERSION I28849.1 GI:1819629  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 489)  
AUTHORS Grabstein, K.H., Anderson, D.M., Eisenman, J.R., Fung, V. and Rauch, C.  
TITLE Epithelium-derived T-cell factor  
JOURNAL Patent: US 5574138-A 1 12-NOV-1996;  
FEATURES Location/Qualifiers  
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1. 489  
BASE COUNT 159 a 79 c 95 g 156 t  
ORIGIN  
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QY 481 ACTTCTTGA 489  
Db 481 ACTTCTTGA 489  
RESULT 12  
LOCUS I62692 489 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 1 from patent US 5660824.  
ACCESSION I62692  
VERSION I62692.1 GI:2480400  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 489)  
AUTHORS Grabstein, K.H., Quinn, L.S. and Trout, A.B.  
TITLE Muscle trophic factor  
JOURNAL Patent: US 5660824-A 1 26-AUG-1997;  
FEATURES Location/Qualifiers  
source  
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BASE COUNT 159 a 79 c 95 g 156 t  
ORIGIN  
Query Match 100.0%; Score 489; DB 6; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.2e-92;  
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Db 481 ACTCTTGA 489

RESULT 13  
I79219  
LOCUS I79219  
DEFINITION Sequence 1 from patent US 5707616.  
ACCESSION I79219  
VERSION I79219.1 GI:3207509  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 489)  
AUTHORS Grabstein, K.H., Anderson, D.M., Eisenman, J.R., Fung V. and Rauch, C.  
TITLE Method for treating or preventing gastrointestinal disease with  
epithelium-derived T-cell factor  
JOURNAL Patent: US 5707616-A 1 13-JAN-1998;  
FEATURES Location/Qualifiers  
source  
BASE COUNT 159 a 79 c 95 g 156 t  
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.2e-92;  
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QY 481 ACTCTTGA 489  
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Db 481 ACTCTTGA 489

RESULT 14  
AR103280  
LOCUS AR103280

DEFINITION Sequence 11 from patent US 6087172.  
ACCESSION AR103280  
VERSION AR103280.1 GI:12814868  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1202)  
AUTHORS Veeorapanen, D., Hatanaka, S. and Nozawa, I.  
TITLE Ribozymes targeted to human IL-15 mRNA  
JOURNAL Patent: US 6087172-A 11 11-JUL-2000;  
FEATURES Location/Qualifiers  
source  
BASE COUNT 355 a 219 c 249 g 379 t  
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 1202;  
Best Local Similarity 100.0%; Pred. No. 9.4e-93;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 481 ACTCTTGA 489  
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Db 797 ACTCTTGA 805

RESULT 15  
AX024715  
LOCUS AX024715  
DEFINITION Sequence 1 from Patent WO0028019.  
ACCESSION AX024715  
VERSION AX024715.1 GI:10184794  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 1202)  
AUTHORS Doudevani, A. and Chaimovitz, C.  
TITLE Antisense oligomer

JOURNAL Patent: WO 0028019-A 1 18-MAY-2000;  
MOR RESEARCH APPLIC LTD (IL) ; DOUDEVANI AMOS (IL) ; UNIV BEN  
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FEATURES Location/Qualifiers  
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BASE COUNT 355 a 219 c 249 g 379 t  
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 1202;  
Best Local Similarity 100.0%; Pred. No. 9.4e-93;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAGAAATTCGAAACACACATTGGAAGTATTTCCATCCAGTGTACTTGTGTTTACTTT 60  
Db 317 ATGAGAAATTCGAAACACACATTGGAAGTATTTCCATCCAGTGTACTTGTGTTTACTTT 376  
QY 61 CTAACAGTCATTTCTAACTGAAGCTGGCATTCATGCTTCATTTGGGCTGTTTCAGT 120  
Db 377 CTAACAGTCATTTCTAACTGAAGCTGGCATTCATGCTTCATTTGGGCTGTTTCAGT 436  
QY 121 GCAGGGCTTCCTAAACACAGACCACTGGGTGAATGTAATAGTCAATTTGAAAAAATTT 180  
Db 437 GCAGGGCTTCCTAAACACAGACCACTGGGTGAATGTAATAGTCAATTTGAAAAAATTT 496  
QY 181 GAAGATCTTATTCAATCTATGCATATTGATGCTACTTTATATACGGAAGTGTGTTTAC 240  
Db 497 GAAGATCTTATTCAATCTATGCATATTGATGCTACTTTATATACGGAAGTGTGTTTAC 556  
QY 241 CCCAGTTGCAAAAGTAACAGCAATGAAGTCTTCTCTGGAGTTACAAAGTTATTTCACTT 300  
Db 557 CCCAGTTGCAAAAGTAACAGCAATGAAGTCTTCTCTGGAGTTACAAAGTTATTTCACTT 616  
QY 301 GAGTCGGGAGATGCAAGTATTTCATGATCAGTAGAATACTCATCATCTACCAACACAC 360  
Db 617 GAGTCGGGAGATGCAAGTATTTCATGATCAGTAGAATACTCATCATCTACCAACACAC 676  
QY 361 AGTTTGTCTTCTTAATGGGAATGTAACAGAACTGGATGCAAGAAATGTGAGGAAGTGGAG 420  
Db 677 AGTTTGTCTTCTTAATGGGAATGTAACAGAACTGGATGCAAGAAATGTGAGGAAGTGGAG 736  
QY 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480  
Db 737 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 796  
QY 481 ACTTCTTGA 489  
Db 797 ACTTCTTGA 805

Search completed: September 19, 2002, 23:20:16  
Job time: 10466 sec



PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;  
 PI Rauch C;

XX WPI; 1995-373556/48.  
 DR P-PSDB; AAR83438.  
 XX

PT Isolated DNA encoding polypeptide with mammalian IL-15 activity - which  
 PT stimulates proliferation and differentiation of T cells, used for  
 PT treating carcinoma(s), melanomas, etc. and viral infections  
 XX  
 XX Claim 36; Page 28-29; 48pp; English.

CC A simian species of IL-15 (sIL-15) was purified and its AA  
 CC sequence and cDNA sequence analysed (see AAR83309, AAR83436,  
 CC AAT00524, AAT00525). Both the simian and the human ORFs encode  
 CC a precursor polypeptide (AAR83436, AAR83438). The precursor  
 CC polypeptides each comprise a 48-AA leader sequence and a sequence  
 CC encoding mature simian or human IL-15 polypeptides. The active  
 CC simian and human IL-15 polypeptides are disclosed in AAR83309 &  
 CC AAR83310 respectively. The invention also comprises other mammalian  
 CC IL-15, including human IL-15, that hybridise to probes defined by  
 CC AAR83438. A plasmid contg. a recombinant clone of human IL-15  
 CC cDNA was deposited with ATCC on Feb. 19 1993 under ATCC 69245.  
 CC The deposit was named 141-hETF. AAR83435 is a mammalian mature  
 CC IL-15 polypeptide. It is a generic sequence which encompasses both  
 CC AAR83309 (simian) and AAR83310 (human) IL-15 mature polypeptides.  
 XX

SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 16; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-117;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTTGGAAACACATTTGAGAGTATTTCCATCCAGTCTACTTGTGTTACTT 60  
 DB 1 atgagaatttcgaaccacatttgagaagtatttccatccagtgctacttggttactt 60  
 QY 61 CTAACAGTCAATTTCTAACAGTGGCATTCATGTCCTTCAATTTGGGCTGTTTCAGT 120  
 DB 61 cttaacagtcattttcttaactgaagctggcattcttcttcttcttcttcttcttctt 120  
 QY 121 GCAGGGCTTCTAAACAGAGCCCACTGGTGAATGTAATAGTATTTGAAAAAATT 180  
 DB 121 gcagggtcttctaaacagagcccaactgggtgaatgtaataagtatttgaaaaaatt 180  
 QY 181 GAAGATCTTATTCATCTATGCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 240  
 DB 181 gaagatcttatttcattctatgctatgctatgctatgctatgctatgctatgctatgct 240  
 QY 241 CCCAGTTCGAAGTAACAGCAATGAAGTCTTCTCTTGGAGTTACAGTTTATTTCACTT 300  
 DB 241 cccagttgcaagtaacagcaatgaagcttcttcttcttcttcttcttcttcttcttctt 300  
 QY 301 GAGTCCGAGATGAAGTATTCATGATACATGATGATGATGATGATGATGATGATGATGAT 360  
 DB 301 gagtccgagatgaagtatttcattgatacagatgatacagatgatacagatgatacagat 360  
 QY 361 AGTTTGTCTTCTAATGGGAATGTAACAGATCTGATGATGATGATGATGATGATGATGAT 420  
 DB 361 agtttgtcttcttaatgggaatgtaacagatctgatacagatgatacagatgatacagat 420  
 QY 421 GAAAAAATATTAAGAAATTTTCAGAGTTTGTACATATTTGTCGAATTTTCATCAAC 480  
 DB 421 gaaaaaataataagaatttttcagagtttgtacatatattgttcccaaatgttccatcaac 480  
 QY 481 ACTTCTTGA 489  
 DB 481 acttcttga 489

RESULT 2  
 AAQ84584

ID AAQ84584 standard; cDNA; 489 BP.  
 XX  
 AC AAQ84584;  
 DT 04-SEP-1995 (first entry)  
 XX  
 DE Human IL-15 clone 141.hETF.  
 XX  
 KW Interleukin-15; IL-15; hIL-15; T-cell growth factor;  
 KW antitumor; virucide; ss.  
 XX  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FH CDS 1..489  
 FT /\*tag= a  
 FT /product= IL-15 precursor  
 FT 1..144  
 FT sig\_peptide  
 FT /\*tag= b  
 FT 145..486  
 FT mat\_peptide  
 FT /\*tag= c  
 FT /product= mature IL-15

XX ZA9402636-A.

XX 28-DEC-1994.

XX 18-APR-1994; 94ZA-0002636.

XX 18-APR-1994; 94ZA-0002636.

XX (IMMV) IMMUNEX CORP.

XX Anderson DM, Eisenman JR, Fung V, Grabstein KH;

XX Rauch C;

XX WPI; 1995-082473/11.

XX P-PSDB; AAR66927.

XX New purified interleukin-15 - which induces T cell proliferation  
 XX and differentiation, used for the treatment of tumours and viral  
 XX infection

XX Disclosure; Page 28-29; 47pp; English.

XX A sIL-15 probe was prepared from isolated simian interleukin-15  
 XX cDNA and used to screen a cDNA library generated from the IMTLH  
 XX cell line derived from human bone marrow stromal cells. Clone  
 XX 141.hETF encoded human IL-15.

XX Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 16; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-117;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTTGGAAACACATTTGAGAGTATTTCCATCCAGTCTACTTGTGTTACTT 60  
 DB 1 atgagaatttcgaaccacatttgagaagtatttccatccagtgctacttggttactt 60  
 QY 61 CTAACAGTCAATTTCTAACAGTGGCATTCATGCTTCAATTTGGGCTGTTTCAGT 120  
 DB 61 cttaacagtcattttcttaactgaagctggcattcttcttcttcttcttcttcttctt 120  
 QY 121 GCAGGGCTTCTAAACAGAGCCCACTGGTGAATGTAATAGTATTTGAAAAAATT 180  
 DB 121 gcagggtcttctaaacagagcccaactgggtgaatgtaataagtatttgaaaaaatt 180  
 QY 181 GAAGATCTTATTCATCTATGCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 240  
 DB 181 gaagatcttatttcattctatgctatgctatgctatgctatgctatgctatgctatgct 240



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FT XX /*tag= b
XX US5552303-A.
XX 03-SEP-1996.
XX 08-MAR-1993; 93US-0031399.
XX 08-MAR-1993; 93US-0031399.
XX (IMMV ) IMMUNEX CORP.
XX
XX Anderson D, Eisenman J, Fung V, Grabstein K, Rauch C;
XX WPI; 1996-412063/41.
XX P-PSDB; AAW07255.
XX
XX New isolated simian and human epithelium-derived T-cell factors -
XX which stimulate the proliferation and/or differentiation of
XX T-lymphocytes and T-cell lines
XX
XX Claim 21: Column 23-24; 22pp; English.
XX
XX This is the nucleotide sequence encoding a human epithelium-derived
XX T-cell factor (ETF). The gene was obtained using a 1.37 kb fragment of
XX the corresp. African green monkey gene (AA742242) as a probe to screen a
XX cDNA library constructed from RNA derived from the IMTLH cell line.
XX This cell line is derived by stable transformation of a human bone
XX marrow stromal cell culture with pSV3neo. From a pool of about 1000 cDNA
XX clones, one clone 141.hETF contained this sequence. ETF is a protein of
XX 15-17 kd which is expressed by epithelial cells and stimulates
XX proliferation and/or differentiation of precursor and/or mature T cells.
XX The protein is therefore useful for promoting long term in vivo culture
XX of T-lymphocytes and T-cell lines.
XX
XX Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 17; Length 489;
Best Local Similarity 100.0%; Pred. No. 5.7e-117;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAACACACATTTGAGAGTATTTCCATCCAGTGTCTACTGTGTTTACTTT 60
DB 1 atgagaatttcgaacacacatttgagaagtatttccatccagtgctactgtgtttacttt 60
QY 61 CTAAACAGTCAATTTCTTAACAGAGTGGCATTCATGCTTCATTTTGGGCTGTTTCACT 120
DB 61 ctaaacagtcattttcttaacagagctggcatttccttcattttggcgctgttcagt 120
QY 121 GCAGGGCTTCCTAAACAGAGCCCACTGGGTGAATGTAATAGTATTTGAAAAAATTT 180
DB 121 gcagggttcctaaacagagcccaactgggtgaatgtaataagtattgaaaaaattt 180
QY 181 GAAGATCTTATTCATCTATGCATATTCATCTACTTTATATACGGAAGTGTCTTCAAC 240
DB 181 gaagatcttattcatctatgcataatcattgctactttatatacggaaagtgtgttcac 240
QY 241 CCCAGTTCGAAAGTAACAGCAATGAAGTGTCTTCTCTGGAGTTACAGTATTTTCACTT 300
DB 241 cccagttcgaaagtaacagcaatgaagtgtcttctctggagttacagatttttcaactt 300
QY 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAAATCTGATCATCTCTAGCAAAACAC 360
DB 301 gagtcggagatgcaagtattcatgatacagtagaataatcgtatcctcagcaacaac 360
QY 361 AGTTTGCTTCTAATGGAATGTACAGATCTGGATGCAAGATGTGAGGAAGTGTGAG 420
DB 361 agtttgcttcttaatggaaatgtacagatctggatgcaagaatgtgaggaaactggag 420
QY 421 GAAAAAATATTAAAGAAATTTTTCAGAGTTTTCGTACATATTTGCCAAATGTTTCATCAAC 480
DB 421 gaaaaaataattaaagaatttttcagagtttttcgtacatatattgcccaaatgttcatcaac 480

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QY 481 ACTTCTTGA 489
DB 481 acttcttga 489

RESULT 5
AAT36635
ID AAT36635 standard; cDNA; 489 BP.
XX
AC AAT36635;
XX
DT 17-NOV-1996 (first entry)
XX
DE Human interleukin-15 cDNA.
XX
KW Interleukin-15; antagonist; mutein; graft versus host disease;
KW allograft; T-cell growth factor; ss.
XX
OS Homo sapiens.
XX
PN WO9626274-A1.
XX
PD 29-AUG-1996.
XX
PF 21-FEB-1996; 96WO-US02520.
XX
PR 22-FEB-1995; 95US-0392317.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Grabstein KH, Paxton RJ, Pettit DK;
XX
DR WPI; 1996-402367/40.
DR P-PSDB; AAR98527.
XX
PT Antagonists of interleukin-15 - are used to treat patients having
PT symptoms of graft-versus-host disease and for prolonging allo:graft
PT survival
XX
PS Disclosure; Page 25; 32pp; English.
XX
CC A cDNA clone (AAT36635) codes for human interleukin-15 (IL-15)
CC (AAR98527), a T-cell growth factor. Muteins of human IL-15 or
CC simian IL-15 (see also AAR98526) are useful as antagonists of IL-15
CC and can be prep. by PCR-mediated mutagenesis of the encoding
CC sequences. Preferred muteins have amino acid substitutions at
CC Asp56 and/or Gln156 of the IL-15 protein that prevent signal
CC transduction. They are useful for treating graft-versus-host
CC disease and for prolonging allograft survival.
XX
SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

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Query Match 100.0%; Score 489; DB 17; Length 489;
Best Local Similarity 100.0%; Pred. No. 5.7e-117;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGAGAAATTCGAACACACATTTGAGAGTATTTCCATCCAGTGTCTACTGTGTTTACTTT 60
DB 1 atgagaatttcgaacacacatttgagaagtatttccatccagtgctactgtgtttacttt 60
QY 61 CTAAACAGTCAATTTCTTAACAGAGTGGCATTCATGCTTCATTTTGGGCTGTTTCACT 120
DB 61 ctaaacagtcattttcttaacagagctggcatttccttcattttggcgctgttcagt 120
QY 121 GCAGGGCTTCCTAAACAGAGCCCACTGGGTGAATGTAATAGTATTTGAAAAAATTT 180
DB 121 gcagggttcctaaacagagcccaactgggtgaatgtaataagtattgaaaaaattt 180
QY 181 GAAGATCTTATTCATCTATGCATATTCATCTACTTTATATACGGAAGTGTCTTCAAC 240
DB 181 gaagatcttattcatctatgcataatcattgctactttatatacggaaagtgtgttcac 240

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QY 241 CCAGTGTGCAAGTAAACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTTATTTCACATT 300  
|||||  
Db 241 ccagttgcaagtaacagcaatgaagtgtcttctcttggagttacaagttatttcactt 300  
  
QY 301 GAGTCGGGAGTCAAGTATTTCATGATACAGTAGAATACTGATCATCTTACGCAACAAC 360  
|||||  
Db 301 gagtcgggagtcagagttatttcattgacagtagaatactgacatctctagcaacaac 360  
  
QY 361 AGTTTCTCTCTTAATGGGAATCTAACAGAACTCTGGAATCAAGAAATCTGAGGAACCTGGAG 420  
|||||  
Db 361 agtttctctcttaatgggaatcttaacagaactctggatgcaagaatgtgaggaactggag 420  
  
QY 421 GAAAAAATAATTAAGAAATTTTGCAGAGTTTGTACATATTGTCCTCAATGTTTCATCAAC 480  
|||||  
Db 421 gaaaaaataattaaagaattttgcagagttttgtacatatgtgtccaaatgtttcatcaac 480  
  
QY 481 ACTTCTTTGA 489  
|||||  
Db 481 acttcttga 489  
  
RESULT 6  
AAT58404  
ID AAT58404 standard; cDNA; 489 BP.  
XX  
AC AAT58404;  
XX  
DT 18-MAR-1997 (first entry)  
XX  
DE Interleukin-15 coding sequence.  
XX  
KW IL-15; interleukin-15; T-cell growth factor; proliferation; stimulate;  
KW muscle growth; differentiation; hypertrophy; treat; atrophy; wasting;  
KW skeletal; cardiac; muscle; congestive heart failure; diabetes-associated;  
KW glucose-intolerance; dyslipidaemia; rhabdomyosarcoma; dystrophy; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..489  
FT /tag= a  
FT /product= IL-15  
XX  
PN WO9637223-Al.  
XX  
PD 28-NOV-1996  
XX  
PF 07-MAY-1996; 96WO-US06423.  
XX  
PR 24-MAY-1995; 95US-0535733.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Grabstein KH, Quinn LS, Troutt AB;  
XX  
DR WPI; 1997-020939/02.  
DR P-PSDB; AAW01658.  
XX  
PT Muscle trophic compsn. contg. interleukin 15 - for treating, e.g.  
PT congestive heart failure, muscle wasting etc.  
XX  
PS Disclosure; Page 12; 22pp; English.  
XX  
CC This sequence encodes human interleukin-15 (IL-15) (see AAW01658), a  
CC known T-cell growth factor that can support proliferation of an  
CC IL-2-dependent cell line, C2L2-2. Compsns. contg. IL-15 to stimulate  
CC muscle growth, differentiation or hypertrophy are claimed. The  
CC stimulation of muscle growth is useful for treating atrophy, or wasting,  
CC in particular, skeletal and cardiac muscle atrophy. The compsns. further  
CC comprises a steroid, growth hormone and insulin-like growth factor.  
CC Congestive heart failure, muscle wasting and diabetes-associated  
CC glucose-intolerance or dyslipidaemia, rhabdomyosarcoma and muscular

CC dystrophy can all be treated by such compsns..  
SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;  
  
Query Match 100.0%; Score 489; DB 18; Length 489;  
Best Local Similarity 100.0%; Pred. No. 5.7e-117;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ATGAGAAATTCGAAACACACATTTGAGAAGTATTTCATCCAGTCTACTTGTCTTACTT 60  
|||||  
Db 1 atgagaatttcgaaacacacatttgagaagtatttcattccacagtgactgttttactt 60  
  
QY 61 CTAACAGTCATTTTCTAACTGAAGTCGCAATTCATTCATTTTGGGCTGTTTCAGT 120  
|||||  
Db 61 ctaaacagtcattttctaaactgaagctggcattcatgtcttcattttgggctgtttcagt 120  
  
QY 121 GCAGGGCTTCCTAAACAGAGCCAACTGGTGAATGTAATTAAGTATTTGAAAAAATTT 180  
|||||  
Db 121 gcagggcttcctaaacagagccaaactgggtgaatgtaataagtatttgaaaaaatt 180  
  
QY 181 GAAGATCTTATTCAATCTATGATATTGATGCTACTTTATATACGGAAAGTGATGTTCCAC 240  
|||||  
Db 181 gaagatcttattcaatctatgcatattgatgctactttatatatacggaaagtgtgttcac 240  
  
QY 241 CCCAGTTGCAAGTAACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTTATTTCACATT 300  
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Db 241 cccagttgcaagtaacagcaatgaagtgtcttctctctgttgagttacaagttatttcactt 300  
  
QY 301 GAGTCGGGAGTCAAGTATTTCATGATACAGTAGAATACTGATCATCTTACGCAACAAC 360  
|||||  
Db 301 gagtcgggagtcagagttatttcattgacagtagaatactgacatctctagcaacaac 360  
  
QY 361 AGTTTCTCTCTTAATGGGAATCTAACAGAACTCTGGAATCAAGAAATCTGAGGAACCTGGAG 420  
|||||  
Db 361 agtttctctcttaatgggaatgttaacagaactctggatgcaagaatgtgaggaactggag 420  
  
QY 421 GAAAAAATAATTAAGAAATTTTGCAGAGTTTGTACATATTGTCCTCAATGTTTCATCAAC 480  
|||||  
Db 421 gaaaaaataattaaagaattttgcagagttttgtacatatgtgtccaaatgtttcatcaac 480  
  
QY 481 ACTTCTTTGA 489  
|||||  
Db 481 acttcttga 489  
  
RESULT 7  
AAV23554  
ID AAV23554 standard; cDNA; 489 BP.  
XX  
AC AAV23554;  
XX  
DT 13-JUL-1998 (first entry)  
XX  
DE Human interleukin-15 coding sequence.  
XX  
KW Human; interleukin-15; IL-15; T cell; B cell; proliferation; vaccine;  
KW cytokine; growth factor; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..489  
FT /\*tag= a  
XX  
PN US5747024-A.  
XX  
PD 05-MAY-1998.  
XX  
PF 19-JUN-1995; 95US-0504042.  
XX  
PR 19-JUL-1995; 95US-0504042.  
PR 08-MAR-1993; 93US-0031399.

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PR 22-APR-1994; 94US-0233606.
PR 22-FEB-1995; 95US-0393305.
XX
XX (IMV ) IMMUNEX CORP.
XX
XX Grabstein KH, Widmer MB;
XX
XX WPI; 1998-285678/25.
XX
XX P-PSDB; AAW53878.
XX
XX Use of Interleukin-15 - to enhance immunogenicity of a vaccine
XX
XX Disclosure; Column 5-6; 5pp; English.
XX
XX This sequence encodes human interleukin-15 (IL-15), which can be used in
XX the vaccine of the invention. The vaccine composition comprises an
XX immunogenic amount of a vaccine antigen (Ag) and an
XX immunogenicity-augmenting amount of IL-15. The composition is useful for
XX enhancing the immunogenicity of a vaccine. The cytokine IL-15 is a potent
XX T and B cell growth factor. It causes proliferation and differentiation
XX of these cells and augments T cell mediated immune responses. The vaccine
XX composition can sufficiently elicit an immune response without being
XX deleterious to the recipient, especially when using pathogenically
XX deficient antigens. Some vaccines do not elicit a strong immune response
XX and cannot provide sufficient protection on further exposure to the
XX antigen.
XX
XX Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 19; Length 489;
Best Local Similarity 100.0%; Pred. No. 5,7e-117;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCAATTCGAAACACCATTTGAGAAGTATTTCCATCCAGTCTACTGTGTTTACTT 60
DB 1 atgagaatttcgaaacacacatttgagaagatttccatccagtcactgtgttactt 60
QY 61 CTAAACAGTCATTTCTTAACAGAACTGGCAATTCATGCTTCTTCAATTTGGGCTGTTTCAGT 120
DB 61 ctaaacagtcattttcttaactgaagctggcattcattgtcttcatttgggctgttccagt 120
QY 121 GCAGGCTTCCTAAACAGAACCCCACTGGGTGATGTAAATAGTATTTGAAAAAATTT 180
DB 121 gcaggcttcctaaacagaaaccccaactgggtgatatgtaataagtgatttgaaaaaatt 180
QY 181 GAAGATCTTATTCATCTATGTCATATTTGATGCTACTTTATATACGAAAGTGCATTTCCAC 240
DB 181 gaagatcttattcaatctatgcatattgatgctactttatatacagaaagtgtttcac 240
QY 241 CCCAGTTCGAAGTAACAGCAATGAAGTGGCTTCTCTTTGGAGTTACAAAGTATTTTCAGTT 300
DB 241 cccagttgcgaagttaacagcaatgaagtggcttctctcttctctggagttacaagtatttcactt 300
QY 301 GAGTCCGAGATGCAAGTATTCATGATACATACAGTACAGTAAATCTGATCATCTAGCAACAC 360
DB 301 gagtccgagatgcaagtatctatgatacagatgataaaaatctgatactctagcaaacac 360
QY 361 AGTTTGTCTTCTAATGGAATGTACAGAACTCTGGATGCAAGAAATGTGAGAACTGGAG 420
DB 361 agtttgtcttctaattggaatgtacagaaactctggatgcaagaaatgtgagaaactggag 420
QY 421 GAAAAAATATTAAGAAATTTTTCAGAGTGTGTTGACATATTTGTCCTCAATGTTTCATCAAC 480
DB 421 gaaaaaataattaagaatttttcagaggtttgtgacatatattgtccaaaatgttcatcaac 480
QY 481 ACTTCTTCA 489
DB 481 acttcttga 489

RESULT 8
AAV02873

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ID AAV02873 standard; DNA; 489 BP.
XX
XX AAV02873;
XX
XX 08-MAY-1998 (first entry)
XX
XX Simian epithelium derived T-cell factor DNA.
XX
XX Epithelium derived T-cell factor; ETF; simian; gastrointestinal disease;
XX B-cell stimulation; epithelium; villi; CD4+; CD8+; T-cell stimulation;
XX treatment; prevention; ss.
XX
XX Simian.
XX
XX Key Location/Qualifiers
XX CDS 1..489
XX FT /*tag= a
XX FT sig_peptide 1..48
XX FT /*tag= b
XX FT mat_peptide 49..486
XX FT /*tag= c
XX FT /*product= ETF
XX FT /*note= "Epithelium-derived T-cell factor"
XX
XX US5707616-A.
XX
XX 13-JAN-1998.
XX
XX 04-OCT-1996; 96US-0726817.
XX
XX 22-FEB-1995; 95US-0393305.
XX 08-MAR-1993; 93US-0031399.
XX 22-APR-1994; 94US-0233606.
XX
XX (IMV ) IMMUNEX CORP.
XX
XX Anderson DM, Eisenman JR, Fung V, Grabstein KH;
XX Rauch C;
XX
XX WPI; 1998-100295/09.
XX
XX P-PSDB; AAW39185.
XX
XX Treatment or prevention of gastrointestinal diseases - by
XX administering epithelium-derived T-cell factor polypeptide
XX
XX Claim 1C; Column 35-36; 34pp; English.
XX
XX This sequence encodes a simian epithelium-derived T-cell factor (ETF)
XX which is used in a method for treating or preventing gastrointestinal
XX disease. These polypeptides have particular application in the treatment
XX of gastrointestinal disorders associated with disruption of the
XX gastrointestinal epithelium or villi such as chemotherapy- and
XX radiation-therapy induced enteritis (gut toxicity), mucositis, peptic
XX ulcer disease, gastroenteritis and colitis, villus atrophic disorders,
XX malignancy and inflammatory bowel disease. ETF polypeptides may also be
XX useful in the treatment of human immunodeficiency virus (HIV) and
XX HIV-associated disease due to their ability to stimulate CD4+ and CD8+
XX cells. Biologically active ETF may be used to treat a variety of other
XX diseases or conditions where T-cell or B cell stimulation is desired.
XX
XX Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 19; Length 489;
Best Local Similarity 100.0%; Pred. No. 5,7e-117;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACACCATTTGAGAAGTATTTCCATCCAGTCTACTGTGTTTACTT 60
DB 1 atgagaatttcgaaacacacatttgagaagatttccatccagtcactgtgttactt 60
QY 61 CTAACAGTCATTTCTTAACAGAACTGGCAATTCATGCTTCTTCAATTTGGGCTGTTTCAGT 120

```



Db 61 ctaaacagtcattttcttaaacagtcgaagctggcattcattgcttcttcatttttgggtgtttcagt 120  
 QY 121 GCAGGGCTTCTTAAACAGAGCCAACTGGTGGTGAATGTATTAAGTGAATTTGAAAAAATT 180  
 Db 121 gcagggtcttcttaaacagagccaaactgggtgaatgtaataagtgatttgaaaaaaatt 180  
 QY 181 GAAGATCTTATTCAAATCGCATATGATGCTGCTACTTTATATACGGAAGTGAATGTCAC 240  
 Db 181 gaagacttattcaactctatgcatattgctgctactttatatacggaaagtgtgtcac 240  
 QY 241 CCAGGTTCGAAAGTAAACAGCAATGAAGTCTTCTTCTGGAGTTACAAGTTATTTCACTT 300  
 Db 241 ccaggttgcgaagttaacagcaatgaagtgtcttctcttggaggtacaagtatttcaact 300  
 QY 301 GAGTCGGAGATCAAGTATTCATGATACAGTAGAGTAAATCTGTATCTCTAGCAACAAC 360  
 Db 301 gagtcggagatgcaagttattcatgatacagtagaagaatctgatactcctcagcaacaac 360  
 QY 361 AGTTTCCTCTTAATCGGAATGTAACAGAAATCTGGATGCAAGAATCTGAGGAACCTGGAG 420  
 Db 361 agttgtcttcttaagtgggaatgtaacagaatctggatgcaagaatgtgaggaaactggag 420  
 QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTGTACATATTCCTCAAAATGTTTCATCAAC 480  
 Db 421 gaaaaaataattaaagaattttgcagagttttgtgacatatattgtccaaaattgttcatcaac 480  
 QY 481 ACTTCTTGA 489  
 Db 481 acttcttga 489

RESULT 9  
 AAX29479  
 ID AAX29479 standard; DNA; 489 BP.  
 AC AAX29479;  
 DT 10-JUN-1999 (first entry)  
 DE Simian epithelium-derived T-cell factor (ETF) encoding DNA.  
 XX Epithelium-derived T-cell factor; ETF; immunoassay; enteritis; ulcer;  
 KW T cell proliferation; gastrointestinal disease; mucositis; colitis;  
 KW gastroenteritis; villus atrophy; malignancy; inflammatory bowel disease;  
 KW human immune deficiency virus; tumour; simian; ss.  
 OS Mammalia.  
 PN US5892001-A.  
 XX  
 PD 06-APR-1999;  
 XX  
 PF 04-OCT-1996; 96US-0725969.  
 XX  
 PR 22-FEB-1995; 95US-0393305.  
 PR 08-MAR-1993; 93US-0031399.  
 PR 22-APR-1994; 94US-0233606.  
 PR 04-OCT-1996; 96US-0725969.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Anderson DM; Eisenman JR, Fung V, Grabstein KH;  
 PI Rauch C;  
 XX  
 DR WPI; 1999-253930/21.  
 DR P-PSDB; AAY03756, AAY03757.  
 XX  
 PT Antibodies specific for epithelium-derived T-cell growth factor  
 XX  
 PS Claim 1; Columns 35-36; 34pp; English.  
 XX  
 CC The invention relates to an isolated antibody that binds specifically to  
 CC a simian or human epithelium-derived T-cell factor (ETF) polypeptide. The

CC antibodies are used, optionally when immobilized or labeled, to detect  
 CC and quantify ETF in standard immunoassays. They may also be used as  
 CC diagnostic and therapeutic agents, e.g. when conjugated to toxins (or  
 CC their precursors) or radionuclides. ETF induces proliferation and/or  
 CC differentiation of T cells (or their precursors), e.g. for use in  
 CC establishing long term in vitro cultures; and is also used to treat  
 CC gastrointestinal disease (e.g. enteritis or mucositis induced by  
 CC chemotherapy or radiation, peptic ulcer, gastroenteritis, colitis,  
 CC villus atrophy, malignancy and inflammatory bowel disease), to treat  
 CC human immune deficiency virus infection or associated disease, or  
 CC generally in any situation requiring stimulation of T or B cell  
 CC proliferation, secretion of immunoglobulins or certain cytokines,  
 CC increased anti-infectious disease immunity, induction of T-cell lytic  
 CC activity or increased destruction of tumour or virus-infected cells. The  
 CC present sequence represents a DNA encoding a simian ETF precursor  
 CC polypeptide sequence.  
 XX  
 SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;  
 Query Match 100.0%; Score 489; DB 20; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-117;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGAGAAATTCGAAACACACATTTGAGAAGTATTTCCATCCAGTCTACTGTGTTACTT 60  
 Db 1 atgagaatttcgaaccacatttgagaagtatttccatccagtgctactgtgttactt 60  
 QY 61 CTAACAGTCATTTCTAACTGAAGCTGGCATTTCATGCTCTTCAATTTGGGCTGTTTCAGT 120  
 Db 61 ctaaacagtcattttcttaaacagtcgaagctgggtcattcctcttcttcttcttctcagt 120  
 QY 121 GCAGGGCTTCTTAAACAGAGCCAACTGGTGGTGAATGTATTAAGTGAATTTGAAAAAATT 180  
 Db 121 gcagggtcttcttaaacagagccaaactgggtgaatgtaataagtgatttgaaaaaaatt 180  
 QY 181 GAAGATCTTATTCAAATCGCATATGATGCTGCTACTTTATATACGGAAGTGAATGTCAC 240  
 Db 181 gaagacttattcaactctatgcatattgctgctactttatatacggaaagtgtgtcac 240  
 QY 241 CCAGGTTCGAAAGTAAACAGCAATGAAGTCTTCTTCTGGAGTTACAAGTTATTTCACTT 300  
 Db 241 ccaggttgcgaagttaacagcaatgaagtgtcttctcttggaggtacaagtatttcaact 300  
 QY 301 GAGTCGGAGATCAAGTATTCATGATACAGTAGAGTAAATCTGTATCTCTAGCAACAAC 360  
 Db 301 gagtcggagatgcaagttattcatgatacagtagaagaatctgatactcctcagcaacaac 360  
 QY 361 AGTTTCCTCTTAATCGGAATGTAACAGAAATCTGGATGCAAGAATCTGAGGAACCTGGAG 420  
 Db 361 agttgtcttcttaagtgggaatgtaacagaatctggatgcaagaatgtgaggaaactggag 420  
 QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTGTACATATTCCTCAAAATGTTTCATCAAC 480  
 Db 421 gaaaaaataattaaagaattttgcagagttttgtgacatatattgtccaaaattgttcatcaac 480  
 QY 481 ACTTCTTGA 489  
 Db 481 acttcttga 489

RESULT 10  
 AAX290032  
 ID AAX290032 standard; cDNA; 489 BP.  
 XX  
 AC AAX290032;  
 XX  
 DT 09-MAY-2000 (first entry)  
 XX  
 DE Human interleukin-15 (IL-15) nucleotide sequence.  
 XX  
 KW Interleukin-15; IL-15; antagonist; irritable bowel disease; IBD;  
 KW celiac disease; treatment; human; ss.

XX Homo sapiens.  
XX WO200002582-A2.  
XX 20-JAN-2000.  
XX 09-JUL-1999; 99WO-GB02201.  
XX P-PSDB; AAY78595.  
XX 10-JUL-1998; 98GB-0014892.  
XX (KENN-) KENNEDY INST RHEUMATOLOGY MATHILDA & TER.  
XX Londel M, Quaratino S, Maiuri L;  
XX WPI; 2000-171080/15.  
XX DR P-PSDB; AAY78595.  
XX Use of antagonists of interleukin-15 for treating an inflammatory bowel  
XX disease, particularly celiac disease -  
XX PS Disclosure; Page 70; 70pp; English.  
XX This sequence represents the human interleukin 15 (IL-15) nucleotide  
XX sequence. The IL-15 nucleotide sequence and the protein encoded by it can  
XX be used to determine and create antagonists of IL-15. An antagonist of  
XX IL-15 can be used for treating an inflammatory bowel disease (IBD). The  
XX invention relates to the treatment of celiac disease using IL-15  
XX antagonists. The antagonists are preferably muteins of IL-15, antibodies  
XX against IL-15 or IL-15 molecules bound to chemical groups that interfere  
XX with the ability of IL-15 to effect a signal transduction through either  
XX the alpha or the gamma subunit of the IL-15 receptor complex. The IL-15  
XX antagonists of the invention can be used to treat irritable bow disease  
XX especially celiac disease.  
XX Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;  
XX

Query Match 100.0%; Score 489; DB 21; Length 489;  
Best Local Similarity 100.0%; Pred. No. 5.7e-117;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACACATTTGAGAGTATTTCCATCCAGTCTACTTGTGTTACTT 60  
DB 1 atgagaatttcgaaccacatttgagagtagtttccatccagtcgtacttgtgttactt 60  
QY 61 CTAACAGTCAATTTCTAAGTGAAGTGGCATTCATGCTCTTCATTTGGGCTGTTTCAGT 120  
DB 61 ctaaacagtcaatTTCTAAGTGAAGTGGCATTCATGCTCTTCATTTGGGCTGTTTCAGT 120  
QY 121 GCAGGGCTTCTAAACAGAGCCCACTGGGTGAATGTAATGAAGTGAATTTGAAAAAAT 180  
DB 121 gcagggtcttctaagagagagcccaactgggtgaatgtaataagtgatttgaaaaaatt 180  
QY 181 GAAGATCTTATTCATCTATCATATTCATCTACTTATATACGGAAGTGAATGTTAC 240  
DB 181 gaagatcttattcatctatcatatTCATCTACTTATATACGGAAGTGAATGTTAC 240  
QY 241 CCCAGTTGCAAGTAACAGCAATGAAGTGTCTTCTTGGAGTTACAGTTATTTCAGTT 300  
DB 241 cccagttgcaagtaaacagcaatgaagtgtcttcttggagttacagttatttcactt 300  
QY 301 GAGTCCGAGATGCAAGTATTTCATGATACAGTAGAATACTGATCATCTAGCAAAACAC 360  
DB 301 gagtccgagatgcaagtatttcatgatacagtagaataactgcatcctcagcaaacac 360  
QY 361 AGTTGTCTCTTAATGGAAGTAAACAGCAATCTGGATCAAGATGAGCACTGGAG 420  
DB 361 agttgtctcttaatggaagttaaacagcaatctggatcaagatgagcaactggag 420  
QY 421 GAAAAAATATTAAAGAAATTTTCAGAGTGTGTTGATATATTTGCCAATGTTTCATCAAC 480  
DB 421 gaaaaaataattaaagaatttttcagaggtgtggtgataattgtcccaattgttcacac 480

QY 481 ACTTCTTGA 489  
DB 481 acttcttga 489  
RESULT 11  
AAZ38244  
ID AAZ38244 standard; cDNA; 489 BP.  
XX AC AAZ38244;  
XX 09-FEB-2000 (first entry)  
XX Simian epithelium-derived T-cell factor (ETF) cDNA.  
XX ETF; epithelium-derived T-cell factor; T-cell; T-lymphocyte;  
XX proliferation; differentiation; growth factor; precursor; mature; CD4+;  
XX CD8+; gastrointestinal; epithelium; cell culture; treatment; HIV;  
XX gastrointestinal disease; gastroenteritis; colitis;  
XX inflammatory bowel disease; villus atrophic disorder; enteritis;  
XX chemotherapy; radiotherapy; gut toxicity; cancer; side effect;  
XX tolerated dose; ss.  
XX Mammalia.  
XX Key Location/Qualifiers  
XX CDS 1..489 /\*tag= a  
XX /\*product= "Simian ETF precursor protein (AAZ52308)"  
XX sig\_peptide 1..144 /\*tag= b  
XX mat\_peptide 145..489 /\*tag= c  
XX /\*product= "Mature simian ETF (AAZ52309)"  
XX US95985262-A.  
XX 16-NOV-1999.  
XX 03-FEB-1997; 97US-0794524.  
XX 22-FEB-1995; 95US-0393305.  
XX 04-OCT-1996; 96US-0726817.  
XX 08-MAR-1993; 93US-0031399.  
XX 22-APR-1994; 94US-0233606.  
XX (IMMV ) IMMUNEX CORP.  
XX Rauch C, Fung V, Eisenman JR, Grabstein KH, Anderson DM;  
XX WPI; 2000-022267/02.  
XX P-PSDB; AAY52308, AAY52309.  
XX Stimulation of T-cells in human immunodeficiency virus infected  
XX patients -  
XX Claim 1; Columns 35-36; 33pp; English.  
XX This sequence represents simian epithelium-derived T-cell factor (ETF)  
XX cDNA. ETF is a previously unidentified T-cell growth factor which  
XX stimulates precursor or mature CD4+ and CD8+ T-lymphocytes to proliferate  
XX and differentiate. It also promotes proliferation of the gastrointestinal  
XX epithelium. The protein can be used to promote long-term in vitro culture  
XX of T-lymphocytes and T-cell lines. ETF can be used for treating HIV  
XX infection, HIV-associated diseases, and other diseases or conditions  
XX where stimulation of T-cell proliferation would be desirable e.g., it  
XX could be used to augment the destruction of tumour cells or virally-  
XX infected cells. ETF may also be used to treat or prevent gastrointestinal  
XX disease, including chemotherapy and radiotherapy associated enteritis,  
XX gastroenteritis, colitis, inflammatory bowel disease and villus atrophic  
XX disorders. Chemotherapy and radiotherapy associated enteritis (gut  
XX toxicity) results in bleeding and sepsis due to gastrointestinal flora



Db 301 gggccgggagcaggtattcatgatacagtagaagaaactgatcatctctagcaacaac 360  
Qy 361 AGTTGCTCTTAATGGGAATTAACAGAAATCTGGATGCAAGAAATGTGAGGAATGGGAG 420  
Db 361 agttgtcttcttaaggaatgaacagaatctggatgcaagaatgtgaggaactggag 420  
Qy 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGTCCAAATGTTCAATCAAC 480  
Db 421 gaaaaaatatgaagaattttgcagagttttgtacatatgtgtccaaatgttcatcaac 480  
Qy 481 ACTTCTTGA 489  
Db 481 actctctga 489

RESULT 13  
AAF57017  
ID AAF57017 standard; cDNA; 489 BP.  
XX  
AC AAF57017;  
XX  
DT 14-MAY-2001 (first entry)  
DE Simian ETF (SETF) polypeptide encoding cDNA.  
XX  
KW Epithelium-derived T-cell factor; ETF; simian; human; enteritis;  
KW gastrointestinal disease; mucositis; peptic ulcer; cytostatic;  
KW villus atrophic disorder; inflammatory bowel disease; antiinflammatory;  
KW anti-HIV; antiviral; T-lymphocyte stimulator; ss.  
XX  
OS Mammalia.

XX FH Key Location/Qualifiers  
FT CDS 1..489  
FT /\*tag= a  
FT /product= "SETF"  
FT sig\_peptide 1..144  
FT /\*tag= b  
FT mat\_peptide 145..486  
FT /\*tag= c  
FT /note= "specifically claimed (see AAB62013)"  
XX US6184359-B1.  
XX PN  
XX PD 06-FEB-2001.  
XX PF 09-NOV-1998; 98US-0189193.  
XX PR 22-FEB-1995; 95US-0393305.  
XX PR 04-OCT-1996; 96US-0725969.  
XX PR 08-MAR-1993; 93US-0031399.  
XX PR 22-APR-1994; 94US-0233606.  
XX PA (IMMV ) IMMUNEX CORP.  
XX PI Grabstein KH, Anderson DM, Eisenman JR, Fung V, Rauch C;  
XX WPI; 2001-217801/22.  
XX DR P-PSDB; AAB62012, AAB62013.

XX PT New antibodies that specifically binds epithelium-derived T-cell factor  
PT polypeptide useful for e.g. treating or preventing gastrointestinal  
PT diseases, HIV and HIV-associated diseases, augmenting destruction of  
PT tumour cells  
XX  
XX Claim 1; Column 35-36; 35pp; English.  
XX  
XX The invention relates to simian and human epithelium-derived T-cell  
XX factor (ETF) polypeptides. Antibodies that specifically bind to the ETF  
XX polypeptides are used for treating or preventing gastrointestinal  
XX diseases, such as chemotherapy and radiation therapy-induced enteritis  
XX and mucositis, peptic ulcer disease, villus atrophic disorders and

CC inflammatory bowel disease; for increasing tolerated doses for radiation  
CC therapy and chemotherapy agents which are limited by gastrointestinal  
CC toxicity; and for treating HIV and HIV-associated diseases. The  
CC antibodies are further used to treat a variety of other diseases or  
CC conditions where it is desired to stimulate proliferation of  
CC T-lymphocytes and B lymphocytes, or the secretion of immunoglobulin B  
CC lymphocytes, to augment anti-infectious disease immunity, to induce CTL,  
CC LAK or NK lytic activity, or to augment the destruction of tumour cells  
CC or cells infected with virus. The present sequence represents a cDNA  
CC encoding the simian ETF (SETF) polypeptide.  
XX  
SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 22; Length 489;  
Best Local Similarity 100.0%; Pred. No. 5.7e-117;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGAGAAATTTGAAACCCACATTTGAGAGTATTTCCATCCAGTGTACTGTGTTACTT 60  
Db 1 atgagaatttgcgaaccacatttgagaagtatttccatccagtgctactgtgttactt 60  
Qy 61 CTAAACAGTCAATTTCTAACTGAAGCTGGCATTCATGCTTTCATTTGGGCTGTTTCAGT 120  
Db 61 ctaaacagtcatttcttaactgaagctgcatcttcttcatttggctgtttcagt 120  
Qy 121 CGAGGGCTTCTTAAACAGAGCCCAACTGGGTGAATGTAAATAGTGATTTGAAAAAATT 180  
Db 121 gcagggtcttctaaacagaagcgaactgggtgaatgtaataagtgatttgaaaaaatt 180  
Qy 181 GAAGATCTTATTCATCTATGATGCTATGCTATGCTATATATATACGGAAGTGATGTTTCA 240  
Db 181 gaagatcttattcaatctatgcatattgctactttatatacaggaagtgatgttcaac 240  
Qy 241 CCCAGTTCGAAGTAACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTTATTTCACTT 300  
Db 241 cccagttgcgaagtaacagcaatgaagtgcttctctctggagtttacaagttatttcaact 300  
Qy 301 GAGTCCGGAGATGCAAGTATTATCATGATACAGTAGAATAATCTGATCATCTAGCAACAAC 360  
Db 301 gagtccggagatgcaagTattcatgatacagtagaataatctgatcatcctagcaacaac 360  
Qy 361 AGTTTGCTTCTTAATGGGAATGTACAGAAATCTGGATGCAAGAAATGTGAGGAATGGAG 420  
Db 361 agttgtcttcttaaggaatgtaacagaactctggatgcaagaatgtgaggaactggag 420  
Qy 421 GAAAAAATATTAAGAAATTTTTCAGAGTGTGACATATTTGTCCAAATGTTTCATCAAC 480  
Db 421 gaaaaaatatgaagaatttttgcagagtttttgcagagttttgcacatatgttccaaatgttcatcaac 480  
Qy 481 ACTTCTTGA 489  
Db 481 acttcttga 489

RESULT 14  
AAX56368  
ID AAX56368 standard; DNA; 1202 BP.  
XX  
AC AAX56368;  
XX  
DT 21-JUL-1999 (first entry)  
XX  
DE Human IL-15 DNA.  
XX  
KW Human; interleukin 15; IL-15; ribozyme; enzymatic RNA; cleavage;  
KW rheumatoid arthritis; inflammatory disorder; ds.  
XX  
OS Homo sapiens.  
XX  
XX WO9923208-A2.  
XX  
PD 14-MAY-1999.

XX	29-OCT-1998;	98WO-IB01837.	XX	AAF21342;
XX	31-OCT-1997;	97US-0962503.	XX	14-MAR-2001 (first entry)
XX	(HISM ) HISAMITSU PHARM CO LTD.		XX	Human low adenosine antisense oligonucleotide related sequence #2909.
XX	Hamanaka S, Nozawa I, Veerapaneni D;		XX	Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
XX	WPI; 1999-313334/26.		XX	human; airway disorder; bronchoconstriction; lung inflammation;
XX	New ribozymes targeted to interleukin-15 mRNA		XX	surfactant depletion; respiratory bronchodilator; antiinflammatory;
XX	Disclosure; Fig 8; 46pp; English.		XX	immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
XX	The present sequence describes an isolated RNA molecule which		XX	respiratory obstruction; pulmonary obstruction; impeded respiration;
XX	specifically cleaves mRNA encoding interleukin 15 (IL-15). The		XX	surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
XX	enzymatic RNA molecules can bind to and cleave mRNA encoding IL-15.		XX	respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
XX	They can be used for treating disorders associated with IL-15 such		XX	pulmonary hypertension; emphysema; pulmonary transplantation rejection;
XX	as inflammatory disorders, e.g. rheumatoid arthritis by inhibiting		XX	chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
XX	the synthesis of IL-15 in lymphocytes and preventing the recruitment		XX	cancer; ss.
XX	and activation of macrophages. They can also be used to develop		XX	Homo sapiens.
XX	transgenic animals which can be used to identify the impact of		XX	WO200062736-A2.
XX	increased or decreased IL-15 levels on a particular pathway or		XX	26-OCT-2000.
XX	phenotype. The present sequence represents a human IL-15 DNA sequence.		XX	24-MAR-2000; 2000WO-US08020.
XX	Sequence 1202 BP; 355 A; 219 C; 249 G; 379 T; 0 other;		XX	06-APR-1999; 99US-0127958.
XX	Query Match 100.0%; Score 489; DB 20; Length 1202;		XX	(UYEC-) UNIV EAST CAROLINA.
XX	Best Local Similarity 100.0%; Pred. No. 7.2e-117; Indels 0; Gaps 0;		XX	(NYCE/) NYCE J W.
XX	Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		XX	Nyce JW;
QY	1 ATGAGATTTCGAAACACATTTGAGAAGTATTTCATCCAGTCGCTACTTGTGTACTT	60	XX	WPI; 2000-679539/66.
Db	317 atgagaatttcgaaccacacatttgagaagatttcctccagtcgactgtgttactt	376	XX	Low adenosine (A) content antisense oligonucleotides which do not
QY	61 CTAAACAGTCATTTCTACTGAAGTCGATTCATCTCTATTTGGCTGTTTCAGT	120	XX	trigger adenosine receptors during metabolism, useful e.g. for treating
Db	377 ctaaacagtcattttctaactgaagctggaagtcatttcatttttggctgttcaag	436	XX	cancers and respiratory obstructions -
QY	121 GCAGGCTTCTCTAAACAGAGCCAACTGGTGAATGTAATGATGTTGAAAAAAT	180	XX	Disclosure; Page 1344-1345; 1592pp; English.
Db	437 gcagggtcttctaaacagagccaaactgggtgaatgaatgaatttgaaaaaatt	496	XX	The present invention describes low adenosine (A) content antisense
QY	181 GAAGATCTTATTCATCTATGCAATATGATGCTACTTTATATACGGAAGTGTTCAC	240	XX	oligonucleotides and compositions (I) comprising them. In the antisense
Db	497 gaagatctttatccaatctatgcatattgatgctactttatatacgaagtgatgtoac	556	XX	oligonucleotides the A is replaced by a 'Universal' or alternative base.
QY	241 CCCAGTTCGAAAGTACACGAATGAGTCTTCTCTTGGAGTTACAGTTATTTCACTT	300	XX	(I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
Db	557 cccagttgcaaaagtaacagcaatgaagtgtcttctcttgaggtacaagtatttcaact	616	XX	immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
QY	301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTAGAATACTGATCATCTAGCAACAAC	360	XX	The antisense oligonucleotides and (I) can be used to down-regulate the
Db	617 gagtcggagatgaagatttcattatgatacagtagaataatctgatactctagcaacaac	676	XX	expression and or activity of target polypeptides associated with
QY	361 AGTTCTCTCTTAATGGGAATGTAACAGATCTGGATGCAAGAATCTGAGGAACGGAG	420	XX	lung/respiratory disorders and malignancies, such as stimulating and
Db	677 agttgcttctaattggaatgtaacagaatctggtgcaagaatgtgaggaactggag	736	XX	activating peptide factors and transmitters, transcription factors,
QY	421 GAAAAAATTAATAAGAAATTTTGCAGAGTTTGTGACATATTTGTCCAATGTTTCATCAAC	480	XX	immunoglobulins and antibodies, antibody receptors, cytokines and
Db	737 gaaaaaataataagaattttgcagagttttgtacattttgtacattttccaaatgttcatcaac	796	XX	chemokines, endogenously produced specific and non-specific enzymes,
QY	481 ACTTCTTGA 489		XX	binding proteins, adhesion molecules and their receptors, cytokine and
Db	797 acttctctga 805		XX	chemokine receptors, adenosine receptors, bradykinin receptors, central
RESULT 15			XX	nervous system (CNS) and peripheral nervous and non-nervous system
AAF21342			XX	transmitters, defensins, growth factors, vasoactive peptides and
ID AAF21342 standard; DNA; 1202 BP.			XX	receptors, binding proteins and malignancy associated proteins. The
			XX	antisense oligonucleotides may be used in this way to treat disorders
			XX	including respiratory obstruction (especially pulmonary obstruction
			XX	and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
			XX	and/or surfactant hypoproduction which are associated with a disease or
			XX	condition selected from pulmonary vasoconstriction, inflammation,
			XX	allergies, asthma, impeded respiration, respiratory distress syndrome
			XX	(RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
			XX	hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
			XX	pulmonary transplantation rejection, pulmonary infections, bronchitis,
			XX	and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
			XX	fragments and antisense oligonucleotides used in the exemplification of
			XX	the present invention.
			XX	Sequence 1202 BP; 355 A; 219 C; 249 G; 379 T; 0 other;

Query Match		100.0%;	Score 489;	DB 21;	Length 1202;
Best Local Similarity		100.0%;	Pred. No. 7.2e-117;		
Matches 489;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATCAGAAATTCGAACACCATTTGAGAAGTATTTCATCCAGTGTCTACTTGTGTTACTT	60		
Db	317	atgagaatttcgaaccacatttgagaagtatttccatccagtgctacttggtttactt	376		
QY	61	CTAAACAGTCATTTCCTAACTGAAGCTGGCATTCATGCTCTTTCATTTGGGCTGTTTCAGT	120		
Db	377	ctaaacagtcattttctaactgaagctggcattcatgtcttcatatttgggctgtttcagt	436		
QY	121	GCAGGGCTTCCTAAACAGAACCCAACTGGGTGAATGTAATTAAGTGAATTTGAAAAAATT	180		
Db	437	gcagggttcctaaacagaagccaactgggtgaatgaatgaatttgaaaaaaatt	496		
QY	181	GAAGATCTTATTCAATCTATGATGCTACTTATATATACGGAAGTGATGTTTCAAC	240		
Db	497	gaagatccttattcaatcctatgcataattgatgctactttatatacggaaagtgtgtcac	556		
QY	241	CCCAGTTGCAAAAGTAACAGCAATGAAGTGTCTTCTTGGAGTTACAAGTTATTTTCACTT	300		
Db	557	cccagttgcaaaagtaacagcaatgaagtgtcttctcttggagttacaagttatttcactt	616		
QY	301	GAGTCGGGAGATGCAAGTATTTCATGATCAGTAGAGAAAATCTGATCATCTCTAGCAAAACAC	360		
Db	617	gagtcgggagatgcaagtattcattatgatacagtagaaaaatctgtatcctcctagcaaaacac	676		
QY	361	AGTTTGTCTTCTAATGGGAATGTAACAGAACTGCTGATGCAAGAAATGTCAGGAAGTGGAG	420		
Db	677	agtttgtcttctcaatg99gaatgtaacagaatctggatgcaagaatgtgaggaactggag	736		
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QY	481	ACTTCTTGA	489		
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Search completed: September 19, 2002, 23:25:03  
Job time: 4503 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 19, 2002, 20:33:45 ; Search time 43.55 Seconds  
(without alignments)  
2758.089 Million cell updates/sec

Title: US-09-196-427-2  
Perfect score: 489  
Sequence: 1 ATGAGATTTCGAACACCA.....TGTTCAACACACTTCTTGA 489

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents.NA.\*  
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2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*  
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6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	489	100.0	489	1 US-08-031-399-4	Sequence 4, Appli
2	489	100.0	489	1 US-08-393-305-1	Sequence 1, Appli
3	489	100.0	489	1 US-08-535-733-1	Sequence 1, Appli
4	489	100.0	489	1 US-08-726-817-1	Sequence 1, Appli
5	489	100.0	489	1 US-08-504-042-4	Sequence 4, Appli
6	489	100.0	489	1 US-08-392-317B-2	Sequence 2, Appli
7	489	100.0	489	2 US-08-725-969-1	Sequence 1, Appli
8	489	100.0	489	2 US-08-794-524-1	Sequence 1, Appli
9	489	100.0	489	3 US-09-134-132-2	Sequence 2, Appli
10	489	100.0	489	4 US-09-134-134A-2	Sequence 2, Appli
11	489	100.0	489	4 US-09-134-456-2	Sequence 2, Appli
12	489	100.0	489	4 US-09-196-427-2	Sequence 2, Appli
13	489	100.0	489	4 US-09-189-193-1	Sequence 1, Appli
14	489	100.0	489	5 PCT-US94-03793-4	Sequence 4, Appli
15	489	100.0	489	5 PCT-US96-06423-1	Sequence 1, Appli
16	489	100.0	1202	3 US-08-962-503-11	Sequence 11, Appli
17	487.4	99.7	489	3 US-08-842-947-5	Sequence 5, Appli
18	481	98.4	489	3 US-08-842-947-7	Sequence 7, Appli
19	465	95.1	489	1 US-08-031-399-1	Sequence 1, Appli
20	465	95.1	489	1 US-08-393-305-4	Sequence 4, Appli
21	465	95.1	489	1 US-08-726-817-4	Sequence 4, Appli
22	465	95.1	489	1 US-08-504-042-1	Sequence 1, Appli
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24	465	95.1	489	2 US-08-725-969-4	Sequence 4, Appli
25	465	95.1	489	2 US-08-794-524-4	Sequence 4, Appli
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Sequence 1, Appli  
Sequence 1, Appli  
Sequence 4, Appli  
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Sequence 12, Appli  
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Sequence 11, Appli  
Sequence 42, Appli

## ALIGNMENTS

RESULT 1  
US-08-031-399-4  
; Sequence 4, Application US/08031399  
; Patent No. 5552303  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: Epithelium-derived T-cell Factor  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/031,399  
; FILING DATE: 19930308  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Launer, Charlene  
; REGISTRATION NUMBER: 33,035  
; REFERENCE/DOCKET NUMBER: 2811  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
; US-08-031-399-4

Query Match 100.0%; Score 489; DB 1; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.6e-124;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 481 ACTTCTTGA 489
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## RESULT 2

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US-08-393-305-1
; Sequence 1, Application US/08393305
; Patent No. 5574138
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,305
; FILING DATE: 22-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McMASTERS, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.409C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; INFORMATION FOR SEQ ID NO: 1:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
US-08-393-305-1
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Query Match 100.0%; Score 489; DB 1; Length 489;

Best Local Similarity 100.0%; Pred. No. 1.6e-124;

Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 481 ACTTCTTGA 489
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Db 481 ACTTCTTGA 489
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## RESULT 3

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US-08-535-733-1
; Sequence 1, Application US/08535733
; Patent No. 5660824
; GENERAL INFORMATION:
; APPLICANT: Quinn, LeBris
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Trout, Anthony B.
; TITLE OF INVENTION: Muscle-Trophic Factor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7, Word 5.1a
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SOFTWARE PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2833  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..489  
US-08-535-733-1

Query Match 100.0%; Score 489; DB 1; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.6e-124; Indels 0; Gaps 0;  
Matches 489; Conservative 0; Mismatches 0;

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QY 481 ACTTCTTGA 489  
DB 481 ACTTCTTGA 489

RESULT 4  
US-08-726-817-1  
Sequence 1, Application US/08726817  
Patent No. 5707616  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June

APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,817  
FILING DATE: 04-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/393,305  
FILING DATE: 22-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.409C2  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..489  
US-08-726-817-1

Query Match 100.0%; Score 489; DB 1; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.6e-124; Indels 0; Gaps 0;  
Matches 489; Conservative 0; Mismatches 0;

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DB 1 ATGAGAAATTCGAAACCCACATTTGAGAAGTATTTCCATCCAGTGCCTACTTGTGTTTACTT 60  
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DB 241 CCCAGTTGCAAAAGTACAGCAATGAAGTGCCTTCTCTTGGAGTTACAAGTTATTTTCACTT 300  
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DB 361 AGTTTCTTCTTAATGGGAATTAACAGAACTGGATGCAAAAGTGTGAGGAACCTGGAG 420

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DB 421 GAAAAAATATTAAGAATTTTTCAGAGTTTGTACATATTTGTCCAAATGTTTCATCAAC 480  
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DB 481 ACTTCTTGA 489  
RESULT 5  
US-08-504-042-4  
; Sequence 4, Application US/08504042  
; Patent No. 5747024  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: Epithelium-derived T-cell Factor  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/504,042  
; FILING DATE: 19-JUL-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/031,399  
; FILING DATE: 08-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Launer, Charlene  
; REGISTRATION NUMBER: 33,035  
; REFERENCE/DOCKET NUMBER: 2811  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
US-08-504-042-4  
Query Match 100.0%; Score 489; DB 1; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.6e-124;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAGATTTTGAACACACATTTGAGAGTATTTCCATCCAGTGTCTACTTGTGTTTACTT 60  
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DB 1 ATGAGATTTTGAACACACATTTGAGAGTATTTCCATCCAGTGTCTACTTGTGTTTACTT 60  
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DB 301 GAGTCCGAGATGCAAGTATTTTCATGATACAGTAGAATAATCTGATCATCTCTAGCAACAC 360  
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DB 421 GAAAAAATATTAAGAATTTTTCAGAGTTTGTACATATTTGTCCAAATGTTTCATCAAC 480  
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DB 481 ACTTCTTGA 489  
RESULT 6  
US-08-392-317B-2  
; Sequence 2, Application US/08392317B  
; Patent No. 5795966  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Paxton, Raymond  
; APPLICANT: Pettit, Dean  
; TITLE OF INVENTION: Antagonists of IL-15  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: Word for Windows 95, 7.0  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/392,317B  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Malaska, Stephen L.  
; REGISTRATION NUMBER: 32,655  
; REFERENCE/DOCKET NUMBER: 2831  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
US-08-392-317B-2  
Query Match 100.0%; Score 489; DB 1; Length 489;

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Best Local Similarity 100.0%; Pred. No. 1.6e-124; Mismatches 0; Indels 0; Gaps 0;
Matches 489; Conservative 0;

QY 1 ATGAGAAATTCGAAACACACATTTGAGAAGTATTTCCATCCAGTGCCTACTTGTGTTACTT 60
Db 1 ATGAGAAATTCGAAACACACATTTGAGAAGTATTTCCATCCAGTGCCTACTTGTGTTACTT 60
QY 61 CTAACAGTCATTTCTAACTGAAGCTGGCAATTCATGCTCTTCAATTTGGGCTGTTTCAGT 120
Db 61 CTAACAGTCATTTCTAACTGAAGCTGGCAATTCATGCTCTTCAATTTGGGCTGTTTCAGT 120
QY 121 GCAGGGCTTCCATAACAGAACCAACTGGTGAATGTAATAGTCAATTTGAAAAAATT 180
Db 121 GCAGGGCTTCCATAACAGAACCAACTGGTGAATGTAATAGTCAATTTGAAAAAATT 180
QY 181 GAAGATCTTATCAATCTATGCTACTTTATATACGGAAGTATGATGTTTCAAC 240
Db 181 GAAGATCTTATCAATCTATGCTACTTTATATACGGAAGTATGATGTTTCAAC 240
QY 241 CCCAGTTGCAAGTAACAGCAATGGAAGTCTTCTCTTGGAGTTACAAGTTATTTCACTT 300
Db 241 CCCAGTTGCAAGTAACAGCAATGGAAGTCTTCTCTTGGAGTTACAAGTTATTTCACTT 300
QY 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAAAAATCTGATCATCTAGCAAAACAAC 360
Db 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAAAAATCTGATCATCTAGCAAAACAAC 360
QY 361 AGTTTCTCTTAATGGGAATGTAAACAGAAATCTGGATGCAAAAGAAATGAGGAACTGGAG 420
Db 361 AGTTTCTCTTAATGGGAATGTAAACAGAAATCTGGATGCAAAAGAAATGAGGAACTGGAG 420
QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTGACATATTTGCCAAATGTTTCATCAAC 480
Db 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTGACATATTTGCCAAATGTTTCATCAAC 480
QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 7
US-08-725-969-1
; Sequence 1, Application US/08725969
; Patent No. 5892001
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/725,969
; FILING DATE: 04-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/393,305
; FILING DATE: 22-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
```

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REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..489
US-08-725-969-1

Query Match 100.0%; Score 489; DB 2: Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-124; Mismatches 0; Indels 0; Gaps 0;
Matches 489; Conservative 0;

QY 1 ATGAGAAATTCGAAACACACATTTGAGAAGTATTTCCATCCAGTGCCTACTTGTGTTACTT 60
Db 1 ATGAGAAATTCGAAACACACATTTGAGAAGTATTTCCATCCAGTGCCTACTTGTGTTACTT 60
QY 61 CTAACAGTCATTTCTAACTGAAGCTGGCAATTCATGCTCTTCAATTTGGGCTGTTTCAGT 120
Db 61 CTAACAGTCATTTCTAACTGAAGCTGGCAATTCATGCTCTTCAATTTGGGCTGTTTCAGT 120
QY 121 GCAGGGCTTCCATAACAGAACCAACTGGTGAATGTAATAGTCAATTTGAAAAAATT 180
Db 121 GCAGGGCTTCCATAACAGAACCAACTGGTGAATGTAATAGTCAATTTGAAAAAATT 180
QY 181 GAAGATCTTATCAATCTATGCTACTTTATATACGGAAGTATGATGTTTCAAC 240
Db 181 GAAGATCTTATCAATCTATGCTACTTTATATACGGAAGTATGATGTTTCAAC 240
QY 241 CCCAGTTGCAAGTAACAGCAATGGAAGTCTTCTCTTGGAGTTACAAGTTATTTCACTT 300
Db 241 CCCAGTTGCAAGTAACAGCAATGGAAGTCTTCTCTTGGAGTTACAAGTTATTTCACTT 300
QY 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAAAAATCTGATCATCTAGCAAAACAAC 360
Db 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAAAAATCTGATCATCTAGCAAAACAAC 360
QY 361 AGTTTCTCTTAATGGGAATGTAAACAGAAATCTGGATGCAAAAGAAATGAGGAACTGGAG 420
Db 361 AGTTTCTCTTAATGGGAATGTAAACAGAAATCTGGATGCAAAAGAAATGAGGAACTGGAG 420
QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTGACATATTTGCCAAATGTTTCATCAAC 480
Db 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTGACATATTTGCCAAATGTTTCATCAAC 480
QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 8
US-08-794-524-1
; Sequence 1, Application US/08794524
; Patent No. 5985262
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
```

```

; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,524
; FILING DATE: 03-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/393,305
; FILING DATE: 22-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.409C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
US-08-794-524-1

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Query Match      100.0%; Score 489; DB 2; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-124;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGAGAAATTCGAAACCCACATTTGAGAGATATTTCCATCCAGTGTACTTGTGTTACTT 60
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Db 1 ATGAGAAATTCGAAACCCACATTTGAGAGATATTTCCATCCAGTGTACTTGTGTTACTT 60
   |||||||
QY 61 CTAACAGCTCATTTCTAACTGAAGCTGGCATTCATGCTTCTTGGGCTGTTTCACT 120
   |||||||
Db 61 CTAACAGCTCATTTCTAACTGAAGCTGGCATTCATGCTTCTTGGGCTGTTTCACT 120
   |||||||
QY 121 GCAGGGCTTCCTAAACAGAGCCCAACTGGGTGAATGAATGAATGAATGAATGAATGAAT 180
   |||||||
Db 121 GCAGGGCTTCCTAAACAGAGCCCAACTGGGTGAATGAATGAATGAATGAATGAATGAAT 180
   |||||||
QY 181 GAAGATCTTATTCATCTATGCAATATTTGATGCTTCTTGGGCTGTTTCACT 240
   |||||||
Db 181 GAAGATCTTATTCATCTATGCAATATTTGATGCTTCTTGGGCTGTTTCACT 240
   |||||||
QY 241 CCCAGTTCGAAAGTAAACAGCAATGAAGTGTCTTCTTGGGCTGTTTCACT 300
   |||||||
Db 241 CCCAGTTCGAAAGTAAACAGCAATGAAGTGTCTTCTTGGGCTGTTTCACT 300
   |||||||
QY 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAATACTGATCATCTAGCAAAACAC 360
   |||||||
Db 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAATACTGATCATCTAGCAAAACAC 360
   |||||||
QY 361 AGTTTGTCTTCTAATGGGAATGTAACAGAACTGGATGCAAGAAATGAGAACTGGAG 420
   |||||||
Db 361 AGTTTGTCTTCTAATGGGAATGTAACAGAACTGGATGCAAGAAATGAGAACTGGAG 420
   |||||||
QY 421 GAAAAAATATTAAGAAATTTTGCAGAGATTTTGTACATATTTGTCCAAATGTTTCATCAAC 480
   |||||||
Db 421 GAAAAAATATTAAGAAATTTTGCAGAGATTTTGTACATATTTGTCCAAATGTTTCATCAAC 480
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QY 481 ACTTCTTGA 489
   |||||||
Db 481 ACTTCTTGA 489

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RESULT 9
US-09-134-132-2
; Sequence 2, Application US/09134132
; Patent No. 6013480
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Paxton, Raymond
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Antagonists of IL-15
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Word for Windows 95, 7.0
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,132
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US/08/392,317
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
US-09-134-132-2

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Query Match      100.0%; Score 489; DB 3; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-124;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGAGAAATTCGAAACCCACATTTGAGAGATATTTCCATCCAGTGTACTTGTGTTACTT 60
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Db 1 ATGAGAAATTCGAAACCCACATTTGAGAGATATTTCCATCCAGTGTACTTGTGTTACTT 60
   |||||||
QY 61 CTAACAGCTCATTTCTAACTGAAGCTGGCATTCATGCTTCTTGGGCTGTTTCACT 120
   |||||||
Db 61 CTAACAGCTCATTTCTAACTGAAGCTGGCATTCATGCTTCTTGGGCTGTTTCACT 120
   |||||||
QY 121 GCAGGGCTTCCTAAACAGAGCCCAACTGGGTGAATGAATGAATGAATGAATGAATGAAT 180
   |||||||
Db 121 GCAGGGCTTCCTAAACAGAGCCCAACTGGGTGAATGAATGAATGAATGAATGAATGAAT 180
   |||||||
QY 181 GAAGATCTTATTCATCTATGCAATATTTGATGCTTCTTGGGCTGTTTCACT 240
   |||||||
Db 181 GAAGATCTTATTCATCTATGCAATATTTGATGCTTCTTGGGCTGTTTCACT 240
   |||||||
QY 241 CCCAGTTCGAAAGTAAACAGCAATGAAGTGTCTTCTTGGGCTGTTTCACT 300
   |||||||
Db 241 CCCAGTTCGAAAGTAAACAGCAATGAAGTGTCTTCTTGGGCTGTTTCACT 300
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QY 301 GAGTCGGGAGATCAAGTATTCATGATACAGTAGAGAAATCTGATCATCCTAGCAACAAC 360
Db 301 GAGTCGGGAGATCAAGTATTCATGATACAGTAGAGAAATCTGATCATCCTAGCAACAAC 360
QY 361 AGTTTCTCTTCTTAATGGGAATGTAAACAGATCTGGATGCAAAAGAAATCTGAGGAACCTGGAG 420
Db 361 AGTTTCTCTTCTTAATGGGAATGTAAACAGATCTGGATGCAAAAGAAATGTGAGGAACCTGGAG 420
QY 421 GAAAAAATAATTAAGAAATTTTTCAGAGATTTTGTACATATTTCCAAATGTTTCATCAAC 480
Db 421 GAAAAAATAATTAAGAAATTTTTCAGAGATTTTGTACATATTTCCAAATGTTTCATCAAC 480
QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 10
US-09-134-134A-2
; Sequence 2, Application US/09134134A
; Patent No. 6185466
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Paxton, Raymond
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Antagonists of IL-15
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Word for Windows 95, 7.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,134A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/392,317
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
US-09-134-134A-2

Query Match 100.0%; Score 489; DB 4; Length 489;
Best Local Similarity 100.0%; Pred No. 1.6e-124; Indels 0; Gaps 0;
Matches 489; Conservative 0; Mismatches 0;

QY 1 ATGAGAAATTCGAAACACATTTGAGAGATTTTCCATCCAGTGCCTACTGTGTTACTT 60
Db 1 ATGAGAAATTCGAAACACATTTGAGAGATTTTCCATCCAGTGCCTACTGTGTTACTT 60
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QY 61 CTAACAGTCATTTTCTTAAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTTCAGT 120
Db 61 CTAACAGTCATTTTCTTAAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTTCAGT 120
QY 121 GCAGGGCTTCTTAAACAGAACCAACTGGTGAATGTAATTAAGTGAATTTGAAAAAAATTT 180
Db 121 GCAGGGCTTCTTAAACAGAACCAACTGGTGAATGTAATTAAGTGAATTTGAAAAAAATTT 180
QY 181 GAAGATCTTATTCATCTATGTCATATTTGATGCTACTTTATATACGGAAGTGTGTTTCAC 240
Db 181 GAAGATCTTATTCATCTATGTCATATTTGATGCTACTTTATATACGGAAGTGTGTTTCAC 240
QY 241 CCCAGTGTCAAGTAACAGCAATGAAGTGTCTTCTCTTGGAGTTACAGTATTTTCACTT 300
Db 241 CCCAGTGTCAAGTAACAGCAATGAAGTGTCTTCTCTTGGAGTTACAGTATTTTCACTT 300
QY 301 GAGTCGGGAGATCAAGTATTCATGATACAGTAGAGAAATCTGATCATCCTAGCAACAAC 360
Db 301 GAGTCGGGAGATCAAGTATTCATGATACAGTAGAGAAATCTGATCATCCTAGCAACAAC 360
QY 361 AGTTTCTCTTCTTAATGGGAATGTAAACAGATCTGGATGCAAAAGAAATGTGAGGAACCTGGAG 420
Db 361 AGTTTCTCTTCTTAATGGGAATGTAAACAGATCTGGATGCAAAAGAAATGTGAGGAACCTGGAG 420
QY 421 GAAAAAATAATTAAGAAATTTTTCAGAGATTTTGTACATATTTCCAAATGTTTCATCAAC 480
Db 421 GAAAAAATAATTAAGAAATTTTTCAGAGATTTTGTACATATTTCCAAATGTTTCATCAAC 480
QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 11
US-09-134-456-2
; Sequence 2, Application US/09134456
; Patent No. 6186783
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Paxton, Raymond
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Antagonists of IL-15
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Word for Windows 95, 7.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,456
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/392,317
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
US-09-134-456-2

Query Match      100.0%; Score 489; DB 4; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-124;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAACACCAATTTGAGAGTATTTCCATCCAGTGTCTACTGTGTTTACTT 60
    |||||||
Db 1 ATGAGAAATTCGAACACCAATTTGAGAGTATTTCCATCCAGTGTCTACTGTGTTTACTT 60
    |||||||

QY 61 CTAACAGTCATTTCTTAACAGCTGCAATTCATGCTTCTTCAATTTTGGCTGTGTTTCA 120
    |||||||
Db 61 CTAACAGTCATTTCTTAACAGCTGCAATTCATGCTTCTTCAATTTTGGCTGTGTTTCA 120
    |||||||

QY 121 GCAGGGCTTCCATAACAGAGCCCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAAT 180
    |||||||
Db 121 GCAGGGCTTCCATAACAGAGCCCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAAT 180
    |||||||

QY 181 GAAGATCTTATTCATCTATGCATATTCATGCTTCTTCAATTTTGGCTGTGTTTCA 240
    |||||||
Db 181 GAAGATCTTATTCATCTATGCATATTCATGCTTCTTCAATTTTGGCTGTGTTTCA 240
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QY 241 CCAGCTTGCMAAGTAACAGCAATGCAATGCTTCTTCAATTTTGGCTGTGTTTCA 300
    |||||||
Db 241 CCAGCTTGCMAAGTAACAGCAATGCAATGCTTCTTCAATTTTGGCTGTGTTTCA 300
    |||||||

QY 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAGAAATCTGATCATCTAGCAAA 360
    |||||||
Db 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAGAAATCTGATCATCTAGCAAA 360
    |||||||

QY 361 AGTTTGTCTTCTTAATGGGAATGTAACAGAACTGGATCAAGAAATGTGAGGA 420
    |||||||
Db 361 AGTTTGTCTTCTTAATGGGAATGTAACAGAACTGGATCAAGAAATGTGAGGA 420
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QY 421 GAAAAAATATTAAGAATTTTTCAGAGTATTTGTACATATTTGTCCAAATGTTCA 480
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Db 421 GAAAAAATATTAAGAATTTTTCAGAGTATTTGTACATATTTGTCCAAATGTTCA 480
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QY 481 ACTTCTTGA 489
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Db 481 ACTTCTTGA 489
    |||||||

RESULT 12
US-09-196-427-2
; Sequence 2, Application US/09196427
; Patent No. 6177079
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Paxton, Raymond
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Antagonists of IL-15
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Word for Windows 95, 7.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/196,427
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/392,317
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-597-0430
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
US-09-196-427-2

Query Match      100.0%; Score 489; DB 4; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-124;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAACACCAATTTGAGAGTATTTCCATCCAGTGTCTACTGTGTTTACTT 60
    |||||||
Db 1 ATGAGAAATTCGAACACCAATTTGAGAGTATTTCCATCCAGTGTCTACTGTGTTTACTT 60
    |||||||

QY 61 CTAACAGTCATTTCTTAACAGCTGCAATTCATGCTTCTTCAATTTTGGCTGTGTTTCA 120
    |||||||
Db 61 CTAACAGTCATTTCTTAACAGCTGCAATTCATGCTTCTTCAATTTTGGCTGTGTTTCA 120
    |||||||

QY 121 GCAGGGCTTCCATAACAGAGCCCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAAT 180
    |||||||
Db 121 GCAGGGCTTCCATAACAGAGCCCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAAT 180
    |||||||

QY 181 GAAGATCTTATTCATCTATGCATATTCATGCTTCTTCAATTTTGGCTGTGTTTCA 240
    |||||||
Db 181 GAAGATCTTATTCATCTATGCATATTCATGCTTCTTCAATTTTGGCTGTGTTTCA 240
    |||||||

QY 241 CCAGCTTGCMAAGTAACAGCAATGCAATGCTTCTTCAATTTTGGCTGTGTTTCA 300
    |||||||
Db 241 CCAGCTTGCMAAGTAACAGCAATGCAATGCTTCTTCAATTTTGGCTGTGTTTCA 300
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QY 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAGAAATCTGATCATCTAGCAAA 360
    |||||||
Db 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAGAAATCTGATCATCTAGCAAA 360
    |||||||

QY 361 AGTTTGTCTTCTTAATGGGAATGTAACAGAACTGGATCAAGAAATGTGAGGA 420
    |||||||
Db 361 AGTTTGTCTTCTTAATGGGAATGTAACAGAACTGGATCAAGAAATGTGAGGA 420
    |||||||

QY 421 GAAAAAATATTAAGAATTTTTCAGAGTATTTGTACATATTTGTCCAAATGTTCA 480
    |||||||
Db 421 GAAAAAATATTAAGAATTTTTCAGAGTATTTGTACATATTTGTCCAAATGTTCA 480
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QY 481 ACTTCTTGA 489
    |||||||
Db 481 ACTTCTTGA 489
    |||||||

RESULT 13
US-09-196-193-1
; Sequence 1, Application US/09189193
; Patent No. 6184359
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
```

APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Seed and Berry  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/189,193  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/393,305  
FILING DATE: 22-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: McWaters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.409C2  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..489  
US-09-189-193-1

Query Match 100.0%; Score 489; DB 4; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.6e-124;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACACATTTGAGAAGTATTTCCATCCAGTGCCTACTGTTTACTT 60  
DB 1 ATGAGAAATTCGAAACACATTTGAGAAGTATTTCCATCCAGTGCCTACTGTTTACTT 60  
QY 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATCTCTTCAATTTGGGCTGTTTCAGT 120  
DB 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATCTCTTCAATTTGGGCTGTTTCAGT 120  
QY 121 GCAGGGCTTCCTAAACAGAGCCAACTGGTGAATGTAATAGTATTTGAAAAAATTT 180  
DB 121 GCAGGGCTTCCTAAACAGAGCCAACTGGTGAATGTAATAGTATTTGAAAAAATTT 180  
QY 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTTATATACGAAAGTATGTTTCAC 240  
DB 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTTATATACGAAAGTATGTTTCAC 240  
QY 241 CCCAGTTGCAAGTACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTATTTTCACTT 300  
DB 241 CCCAGTTGCAAGTACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTATTTTCACTT 300  
QY 301 GAGTCCGGAGATCAAGTATTCATGATACAGTAGAAAACTGTATCTCTAGCAACAAC 360  
DB 301 GAGTCCGGAGATCAAGTATTCATGATACAGTAGAAAACTGTATCTCTAGCAACAAC 360  
QY 361 AGTTCTCTTCTTAATGGGAATGTAACAGAAATCTGGATGCAAGAATCTGAGGAACCTGGAG 420  
DB 361 AGTTCTCTTCTTAATGGGAATGTAACAGAAATCTGGATGCAAGAATCTGAGGAACCTGGAG 420

QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 480  
DB 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 480  
QY 481 ACTTCTTGA 489  
DB 481 ACTTCTTGA 489  
RESULT 14  
PCT-US94-03793-4  
Sequence 4. Application PC/TUS9403793  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: Interleukin-15  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/03793  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauener, Charlene  
REGISTRATION NUMBER: 33,035  
REFERENCE/DOCKET NUMBER: 2811  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..489  
PCT-US94-03793-4

Query Match 100.0%; Score 489; DB 5; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.6e-124;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACACATTTGAGAAGTATTTCCATCCAGTGCCTACTGTTTACTT 60  
DB 1 ATGAGAAATTCGAAACACATTTGAGAAGTATTTCCATCCAGTGCCTACTGTTTACTT 60  
QY 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATCTCTTCAATTTGGGCTGTTTCAGT 120  
DB 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATCTCTTCAATTTGGGCTGTTTCAGT 120  
QY 121 GCAGGGCTTCCTAAACAGAGCCAACTGGTGAATGTAATAGTATTTGAAAAAATTT 180  
DB 121 GCAGGGCTTCCTAAACAGAGCCAACTGGTGAATGTAATAGTATTTGAAAAAATTT 180  
QY 181 GAGATCTTATTCATCTATGATATTTGATGCTACTTTATATACGGAAGTATGTTTCAC 240





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 19, 2002, 20:23:50 ; Search time 1617.81 Seconds  
(without alignments)  
4079.596 Million cell updates/sec

Title: US-09-196-427-2  
Perfect score: 489  
Sequence: 1 ATGAGATTTCGAACACCA.....TGTTCAACACACWCTTCTGA 489

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estinu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	489	100.0	982	9	AL548180
2	430.2	88.0	994	9	AL572832
3	399.4	81.7	509	9	AA463370
4	348.8	71.3	800	10	BG184658
5	295.8	60.5	637	9	AI860008
6	292	59.7	756	10	BI832895
7	244	49.9	872	10	BI758686
8	210.6	43.1	826	10	BI685688
9	176.2	36.0	309	10	BF095213
10	174	35.6	471	10	N76741
11	166.6	34.1	690	9	AI596704
12	152.8	31.2	474	10	N49734
13	150.2	30.7	538	9	AI152482
14	150	30.7	515	10	BF704348
15	148.2	30.3	564	9	AA863763
16	139.6	28.5	631	9	BB661271
17	132.4	27.1	166	10	BF379349

18	116	23.7	181	9	AA497102
19	107.2	21.9	817	10	BI756810
20	106.2	21.7	590	9	AA544986
21	105.8	21.6	458	9	BB825167
22	103.2	21.1	430	9	AA858938
23	98.2	20.1	420	10	BE90327
24	90	18.4	550	10	BE98667
25	87.6	17.9	429	9	AA863979
26	86.2	17.6	648	9	AA874636
27	86	17.6	718	10	BI766231
28	83	17.0	434	9	AI503618
29	82	16.8	494	9	AW804168
30	75.6	15.5	405	9	AW121368
31	75.4	15.4	301	10	BF088290
32	74.4	15.2	509	9	AI120615
33	73.8	15.1	275	10	BF088272
34	72	14.7	483	9	AW804165
35	56	11.5	391	12	AZ334843
36	55.8	11.4	278	9	BE177883
37	49.8	10.2	987	12	CNS014PQ
38	44	9.0	1101	12	CNS0039G
39	43.2	8.8	740	10	BM167297
40	43	8.8	1310	12	CNS015ZW
41	42.4	8.7	1204	12	CNS016E2
42	42.2	8.6	1101	12	CNS000MZ
43	42	8.6	1101	12	CNS017KX
44	41.2	8.4	1010	12	CNS07BNJ
45	41	8.4	998	12	CNS00LOZ

#### ALIGNMENTS

RESULT 1

AL548180

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

Source

1. .982

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="CSODI034Y009"

/clone\_lib="LTI\_NFL006\_PL2"

/tissue\_type="placenta"

/notes="Vector: pCMVSPORT 6; Site\_1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by

Life Technologies. Contact : Feng Liang Life technologies,

a division of Invitrogen 9800 Medical Center Drive

Rockville, Maryland 20850, USA Fax : (1) 301 610 8371

Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com"

BASE COUNT 275 a 208 c 214 g 284 t

ORIGIN

1 others

AL548180 982 bp mRNA linear EST 16-FEB-2001  
AL548180 LTI\_NFL006\_PL2 Homo sapiens cDNA clone CSODI034Y009 5

prime, mRNA sequence.

AL548180

AL548180.1 GI:12882943

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

Query Match 100.0%; Score 489; DB 9; Length 982;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-104;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACACATTTGAGAACTATTTCATCCAGTGCCTGCTTACCTT 60  
 Db 358 ATGAGAAATTCGAAACACATTTGAGAACTATTTCATCCAGTGCCTGCTTACCTT 417

QY 61 CTAAACAGTCATTTCTAACTGAAGCTGCATTCATCTCTTCTTGGGCTGTTTCAGT 120  
 Db 418 CTAAACAGTCATTTCTAACTGAAGCTGCATTCATCTCTTCTTGGGCTGTTTCAGT 477

QY 121 CGAGGCTTCCTAAACAGAGCCAACTGGTGAATGTAATAGTGAATTTGAAAAAAT 180  
 Db 478 CGAGGCTTCCTAAACAGAGCCAACTGGTGAATGTAATAGTGAATTTGAAAAAAT 537

QY 181 GAAGATCTTATCAATCTATGATATGATGCTACTTTATATACGGAAGTGTTCAC 240  
 Db 538 GAAGATCTTATCAATCTATGATATGATGCTACTTTATATACGGAAGTGTTCAC 597

QY 241 CCCAGTGCAGAACTAACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTTATTTCACTT 300  
 Db 598 CCCAGTGCAGAACTAACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTTATTTCACTT 657

QY 301 GAGTCGGAGATGCAAGTATTCATGATACAGTACAGTAAATCTCATCATCTAGCAACAAC 360  
 Db 658 GAGTCGGAGATGCAAGTATTCATGATACAGTACAGTAAATCTCATCATCTAGCAACAAC 717

QY 361 AGTTGTCTCTTAATGGGAATGTAACAGAACTGGAATGCAAGAAATGTCAGCACTGGAG 420  
 Db 718 AGTTGTCTCTTAATGGGAATGTAACAGAACTGGAATGCAAGAAATGTCAGCACTGGAG 777

QY 421 GAAAAAATTAATAAGAAATTTTTCAGAGTTTTGTACATATTGTCCAAATGTTTCATCAAC 480  
 Db 778 GAAAAAATTAATAAGAAATTTTTCAGAGTTTTGTACATATTGTCCAAATGTTTCATCAAC 837

QY 481 ACTTCTTGA 489  
 Db 838 ACTTCTTGA 846

RESULT 2  
 AL572832/C  
 LOCUS AL572832 LTI\_NFL006\_PL2 994 bp mRNA linear EST 16-FEB-2001  
 DEFINITION prime, mRNA sequence.  
 ACCESSION AL572832  
 VERSION AL572832.1 GI:12931481  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 994)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES  
 source  
 1..994  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="CSODI034Y009"  
 /clone\_lib="LTI\_NFL006\_PL2"  
 /tissue\_type="placenta"  
 /note="vector: pcMVSPORT 6; Site\_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6

vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 333 a 186 c 154 g 316 t 5 others  
 ORIGIN

Query Match 88.0%; Score 430.2; DB 9; Length 994;  
 Best Local Similarity 98.6%; Pred. No. 1e-90; 2; Indels 0; Gaps 0;  
 Matches 429; Conservative 4; Mismatches 2;

QY 55 TTACTTCTAAACAGTCATTTCTAACTGAAGCTGGCATTCATCTCTTCTTGGGCTGT 114  
 Db 994 TTACTTCTAAACAGTCATTTCTAACTGAAGCTGGCATTCATCTCTTCTTGGGCTGT 935

QY 115 TTCACTGCGAGGCTTCCTAAACAGAGCCAACTGGTGAATGTAATAGTGAATTTGAAA 174  
 Db 934 TTCACTGCGAGGCTTCCTAAACAGAGCCAACTGGTGAATGTAATAGTGAATTTGAAA 875

QY 175 AAAATTGAAGATCTTATCAATCTATGATATGATGCTACTTTATATACGGAAGTGT 234  
 Db 874 AAAATTGAAATCTTATCAATCTATGATATGATGCTACTTTATATACGGAAGTGT 815

QY 235 GTTACCCCGAGTTCGAAAGTAAACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTTAT 294  
 Db 814 GTTACCCCGAGTTCGAAAGTAAACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTTAT 755

QY 295 TCACCTGAGTCGGAGATGCAAGTATTCATGATACAGTAAATCTCATCATCTAGCA 354  
 Db 754 TCACCTGAGTCGGAGATGCAAGTATTCATGATACAGTAAATCTCATCATCTAGCA 695

QY 355 AACACAGTCTCTCTTAATGGGAATGTAACAGAACTGGAATGCAAGAAATGTCAGGAA 414  
 Db 694 AACACAGTCTCTCTTAATGGGAATGTAACAGAACTGGAATGCAAGAAATGTCAGGAA 635

QY 415 CTGGAGGAAAAAATTAATAAGAAATTTTTCAGAGTTTTGTACATATTGTCCAAATGTT 474  
 Db 634 CTGGAGGAAAAAATTAATAAGAAATTTTTCAGAGTTTTGTACATATTGTCCAAATGTT 575

QY 475 ATCAACACTTCTTGA 489  
 Db 574 ATCAACACTTCTTGA 560

RESULT 3  
 AA463370  
 LOCUS AA463370  
 DEFINITION zzx97d12.r1 Soares\_NHMPu\_S1 Homo sapiens cDNA clone IMAGE:811703 5', similar to SW:IL15\_HUMAN P40933 INTERLEUKIN-15 PRECURSOR ;, mRNA sequence.  
 ACCESSION AA463370  
 VERSION AA463370.1 GI:2188254  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 509)  
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, C., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theisling, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.  
 TITLE WashU-Merck EST Project 1997  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu



```

RESULT 5
AI860008/c
LOCUS      637 bp      mRNA      linear      EST 07-MAR-2000
DEFINITION  wm22903.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2436724 3'
              similar to SW:IL15_HUMAN F40933 INTERLEUKIN-15 PRECURSOR ;, mRNA
              sequence.
ACCESSION  AI860008
VERSION    AI860008.1 GI:5513624
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 637)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 3944 Std Error: 0.00
            Seq primer: -400p from Glbco
            High quality sequence stop: 410.
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                /tissue_type="serous papillary carcinoma, high grade, 2
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                /lab_host="DH10B"
                /note="Organ: uterus; Vector: PCMV-SPORT6; Site_1: SalI;
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                Average insert size 1.48 kb. Life Technologies catalog #:
                11542-016"
BASE COUNT 207 a 111 c 91 g 227 t 1 others
ORIGIN

Query Match 60.5%; Score 295.8; DB 9; Length 637;
Best Local Similarity 99.0%; Pred. No. 3e-59;
Matches 297; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 190 ATTCAATCTATGATGCTACTTTATATACGGAAGTGTGTCACCCAGTTGC 249
Db 637 ATTCAATCTATGATGCTACTTTATATACGGAAGTGTGTCACCCAGTTGC 578
QY 250 AAGTAAACAGCAATGAAGTCTTCTCTGGAGTTACAAAGTTATTTCACCTTGAGTCCGGA 309
Db 577 AAGTANCAGCAATGAAGTCTTCTCTGGAGTTACAAAGTTATTTCACCTTGAGTCCGGA 518
QY 310 GATCGAAGTATTATGATACAGTAGAAAATCTGATCATCTAGCAAAACACAGTTTGCT 369
Db 517 GATCGAAGTATTATGATACAGTAGAAAATCTGATCATCTAGCAAAACACAGTTTGCT 458
QY 370 TCTATGGAATGTAACAGATCTGGATGCAAGAAATCTGAGGAAGTGGAGGAAAAAAT 429
Db 457 TCTATGGAATGTAACAGATCTGGATGCAAGAAATCTGAGGAAGTGGAGGAAAAAAT 398
QY 430 ATTAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAACACATCTTGA 489
Db 397 ATTAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAACACATCTTGA 338

RESULT 6
BI832895
LOCUS      756 bp      mRNA      linear      EST 04-OCT-2001
DEFINITION  603082478F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5221771 5',
              mRNA sequence.
ACCESSION  BI832895
VERSION    BI832895.1 GI:1594445
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 756)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
JOURNAL    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11557 row: k column: 20
            High quality sequence stop: 756.
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                /clone="IMAGE:5221771"
                /clone_lib="NIH_MGC_120"
                /lab_host="DH10B"
                /note="Organ: pooled pancreas and spleen; Vector:
                PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                source anonymous pool of spleen and pancreas from 28 yo
                male. Library is oligo-dT primed and directionally cloned
                (EcoRV site is destroyed upon cloning). Average insert
                size 1.5 kb, insert size range 1-2.5 kb. Library is
                normalized and enriched for full-length clones and was
                constructed by C. Gruber (Invitrogen). Research Genetics
                tracking code 025. Note: this is a NIH_MGC Library."
BASE COUNT 247 a 115 c 143 g 251 t
ORIGIN

Query Match 59.7%; Score 292; DB 10; Length 756;
Best Local Similarity 99.4%; Pred. No. 2.4e-58;
Matches 314; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 174 AAAAATTGAAGATCTTATTCATCTATGATGCTACTTTATATACGGAAGTGA 233
Db 1 AAAAATTGAAGATCTTATTCATCTATGATGCTACTTTATATACGGAAGTGA 60
QY 234 TGTTCACCCAGTTGCAAGTAACAGCAATGAAGTCTTCTTGGAGTTACAAGTTAT 293
Db 61 TGTTCACCCAGTTGCAAGTAACAGCAATGAAGTCTTCTTGGAGTTACAAGTTAT 120
QY 294 TTTCACTTGAAGTCCGAGATGCAAGTATTTCATGATACAGTAGAAAATCTGATCATCTAGC 353
Db 121 TTTCACTTGAAGTCCGAGATGCAAGTATTTCATGATACAGTAGAAAATCTGATCATCTAGC 180
QY 354 AAAACAAGTTTGTCTCTTAATGGAATGTAACAGATCTGGATGCAAGTAATGTGGA 413
Db 181 AAAACAAG-TTGTCTCTTAATGGAATGTAACAGATCTGGATGCAAGTAATGTGGA 239
QY 414 ACTGAGGAAAAAATATTAAGAAATTTTTCAGAGTTTGTACATATTGTCCAAATGTT 473
Db 240 ACTGAGGAAAAAATATTAAGAAATTTTTCAGAGTTTGTACATATTGTCCAAATGTT 298

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QY 474 CATCAACACTTCTTGA 489
Db 299 CATCAACACTTCTTGA 314

RESULT 7
BI758686
LOCUS 6034240F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5194977 5',
DEFINITION mRNA sequence.
ACCESSION BI758686
VERSION BI758686
KEYWORDS EST, human.
SOURCE Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 872)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11487 row: 0 column: 10
High quality sequence start: 24
High quality sequence stop: 859.
High quality sequence stop: 859.
Location/Qualifiers
1. .872
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5194977"
/clone_lib="NIH_MGC_114"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."
BASE COUNT 200 a 222 c 227 g 223 t
ORIGIN

Query Match 49.9%; Score 244; DB 10; Length 872;
Best Local Similarity 98.9%; Pred. No. 4.1e-47;
Matches 277; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

QY 1 ATGAGATTTTCCGAACACATTTGAGAAGTATTTCCATCCAGTCTACTTGTGTTACTT 60
Db 592 ATGAGATTTTCCGAACACACATTTGAGAAGTATTTCCATCCAGTCTACTTGTGTTACTT 651
QY 61 CTAACAGTCTATTTCTTAAGTGAAGCTGGCATTCATGCTTCATTTGGGCTGTTTCAGT 120
Db 652 CTAACAGTCTATTTCTTAAGTGAAGCTGGCATTCATGCTTCATTTGGGCTGTTTCAGT 711
QY 121 GCAGGGCTTCTTAAACAGAACCACTGGGTGAATGAATGAAGTATTTGA-AAAAAAT 179
Db 712 GCAGGGCTTCTTAAACAGAACCACTGGGTGAATGAATGAAGTATTTGA-AAAAAAT 771
QY 180 TGAAGATCTTATCAATCTATGATATTTATGCTACTTTATATACGGAAGTATGTTCA 239
Db 772 TGAAGATCTTATCAATCTATGATATTTATGCTACTTTATATACGGAAGTATGTTCA 831

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QY 240 -CCCCAGTTCCAAAGTAACA-GCAATCAAGTCTTCTCT 277
Db 832 CCCCCAGTTCCAAAGTAACAAGCAATGAAGTCTTCTCT 871

RESULT 8
BI685688
LOCUS 603309529F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5345382 5',
DEFINITION mRNA sequence.
ACCESSION BI685688
VERSION BI685688
KEYWORDS EST, house mouse.
SOURCE Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 826)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11877 row: j column: 07
High quality sequence stop: 826.
High quality sequence stop: 826.
Location/Qualifiers
1. .826
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5345382"
/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT 212 a 218 c 174 g 222 t
ORIGIN

Query Match 43.1%; Score 210.6; DB 10; Length 826;
Best Local Similarity 79.4%; Pred. No. 2.7e-39;
Matches 274; Conservative 0; Mismatches 69; Indels 2; Gaps 2;

QY 1 ATGAGATTTTCCGAACACATTTGAGAAGTATTTCCATCCAGTCTACTTGTGTTACTT 60
Db 481 ATGAGATTTTCCGAACACATTTGAGAAGTATTTCCATCCAGTCTACTTGTGTTACTT 540
QY 61 CTAACAGTCTATTTCTTAAGTGAAGCTGGCATTCATGCTTCATTTGGGCTGTTTCAGT 120
Db 541 CTAACAGTCTATTTCTTAAGTGAAGCTGGCATTCATGCTTCATTTGGGCTGTTTCAGT 599
QY 121 GCAGGGCTTCTTAAACAGAACCACTGGGTGAATGAATGAAGTATTTGA-AAAAAAT 180
Db 600 GTAGGTCTCCCTAAACAGAACCACTGGGTGAATGAATGAAGTATTTGA-AAAAAAT 659
QY 181 GAAGATCTTATCAATCTATGATATTTATGCTACTTTATATACGGAAGTATGTTCA 240
Db 660 GAAGATCTTATCAATCTATGATATTTATGCTACTTTATATACGGAAGTATGTTCA 718
QY 241 CCCAGTTTCCAAAGTAACAAGTGAAGTCTTCTTCTTGGAGTTTACAAGTATTTCACTT 300

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Db	121	TATTAAGAATTTTGCAGAGTTTTGTACATATTGCCAAATGTTCAACACTTCTTG	180
QY	489	A 489	
Db	181	A 181	
RESULT	10		
N76741			
LOCUS			
DEFINITION			
ACCESSION	N76741	471 bp	linear
VERSION			EST 02-APR-1996
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
Source			
BASE COUNT	161 a	68 c	83 g 154 t 5 others
ORIGIN			
Query Match	35.6%	Score 174;	DB 10; Length 471;
Best Local Similarity	97.4%;	Pred. No. 9.8e-31;	
Matches 185;	Conservative	0; Mismatches 4;	Indels 1; Gaps 1;
QY	301	GAGTCCGGAGATCGAAGTATTCATGATACAGTAAAGAAATCTGATCATCTTCAGCAACAC	360
Db	4	GAGTCCGGAGATCGAAGTATTCATGATACAGTAAAGAAATCTGATCATCTTCAGCAACAC	63

Qy	361	AGTTTGTCTTCTTAATGGAATGTAAACAGAACTCTGGATGCAAAAGAAATGTGAGGAACCTGGAG	420
Db	64	AGTTTGTCTTCTTAATGGAATGTAAACAGAACTCTGGATGCAAAAGAAATGTGAGGAACCTGGAG	123
Qy	421	GAAGAAATATTAAGAATATTTTCGACAGATTTTGTACATATGTCCTCAATGTTTCAT-CAA	479
Db	124	GAAGAAATATTAAGAATATTTTCGACAGATTTTGTACATATGTCCTCAATGTTTCAT-CAA	183
Qy	480	CACCTCTTTGA	489
Db	184	CACCTCTTTGA	193
RESULT	11		
LOCUS	AI596704		
DEFINITION	VK38h11.v1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:948933 5' similar to gb:U14332 Mus musculus interleukin 15 (MOUSE)), mRNA sequence.	690 bp	mRNA linear EST 21-APR-1999
ACCESSION	AI596704		
VERSION	AI596704		
KEYWORDS	EST		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 690)		
AUTHORS	NCI-CCAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
JOURNAL	Unpublished (1997)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgaps-remail.nih.gov">cgaps-remail.nih.gov</a> This clone is available royalty-free through LLNL ; contact the IMAGE Consortium ( <a href="mailto:info@image.llnl.gov">info@image.llnl.gov</a> ) for further information. MG1:545789 This read is a RESSEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the correct orientation) Seq primer: -40RP from Gibco High quality sequence stop: 466.		
FEATURES	Location/Qualifiers		
source	1..690		
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	/strain="C57BL/6J"		
	/db_xref="taxon:10090"		
	/clone="IMAGE:948933"		
	/clone_lib="Soares_mammary_gland_NbMMG"		
	/sex="male"		
	/tissue_type="mammary gland"		
	/dev_stage="4 weeks"		
	/lab_host="DH10B"		
	/notes="Organ: mammary gland; Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5']		
	TCGTACCAATCTGAATGGGAGCGCGCGAATGGTTTTTTTTTTTTTTTTTTTTTTTTTTT		
	T 3'; double-stranded cDNA was ligated to Eco RI		
	adaptors (Pharmacia), digested with Not I and cloned into		
	the Not I and Eco RI sites of the modified p7T3 vector.		
	RNA provided by Dr. Minoru Ko, Wayne State Univ. Library		
	constructed and normalized by. Bento Soares and M.Fatima		
	Bonaldo."		
BASE COUNT	178 a 177 c 158 g 170 t	7 others	
ORIGIN			
Query Match	34.1%	Score 166.6; DB 9; Length 690;	
Best Local Similarity	81.5%	Pred. No. 5.4e-29;	
Matches 190;	Conservative	0; Mismatches 43; Indels 0; Gaps 0;	
Qy	1	ATGAGATTTTCGAACACACATTTTGAGAAGATTTTCCTCCAGTGTACTTGTGTTTACTT	60



		Matches	185;	Conservative	0;	Mismatches	58;	Indels	0;	Gaps	0;
Best Local Similarity 76.1%; Pred. No. 3.7e-25;											
QY	247	TGCAAGATACAGCAATGAAGTGCCTTTCTCTGGAGTTACAAGTTATTTCACTTGAGTCC	306								
Dd	532	TGAAAGTTACTGCAATGAAGTCTCTCCCTCGAATTGCCAATTATTTACATGAGTAC	473								
QY	307	GGAGATGCAAGTATTCAATGATACAGTAGAAAATCTGATCATCCTAGCAAAACACAGTTTG	366								
Dd	472	AGTAACATGACTCTTAATGAACACAGTAGAAGCGTGCTTACCCTTGCAAACAGCACCTGTG	413								
QY	367	TCCTTAATGGGAATGTAAACAGAATCTGGATGCAAAAGAAATGTGAGGAACCTGGAGAAAAA	426								
Dd	412	TCCTTCAACAGAAATGTAGCAGAAATCTGGCTGCAAGGAATCTGAGGAGCTGGAGGAGAAA	353								
QY	427	AATATTAAAGAAATTTTTGCAGAGTTTTGTACATATTGTCCAAATGTTTCATCAACACTTCT	486								
Dd	352	ACCTTCACAGAGTTTTTGCAAGCTTTATACGCATTGTCCAAATGTTTCATCAACACAGTCC	293								
QY	487	TGA	489								
Dd	292	TGA	290								

RESULT 14	
BF704348/C	
LOCUS	515 bp mRNA linear EST 22-DEC-2000
DEFINITION	MI-P-03-aba-f-02-1-UM.s1 MI-P-03 Sus scrofa cDNA clone
ACCESSION	MI-P-03-aba-f-02-1-UM 3', mRNA sequence.
VERSION	BF704348
KEYWORDS	BF704348.1 GI:11989750
SOURCE	EST.
ORGANISM	pig.
REFERENCE	Sus scrofa
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
COMMENT	1 (bases 1 to 515)
	Bonaldo,M.F., Lennon,G. and Soares,M.B.
	Normalization and subtraction: two approaches to facilitate gene
	discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
MEDLINE	97044477
COMMENT	Contact: Tuggle CK
	Molecular Genetics Laboratory, Department of Animal Science
	Iowa State University
	201 Kildee Hall, Ames, IA 50011-3150, USA
	Tel: 5152944252
	Fax: 5152942401
	Email: cktuggle@iastate.edu
	The sequence contained an oligo-dT track that was present in the
	oligonucleotide that was used to prime the synthesis of first

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strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
non-normalized ovary at estrus day 12 library cDNA library
Preparation: RJ Woods, JA Green, KS Prather S142 Animal Science
Research Center, Department of Animal Science, University of
Missouri-Columbia, 55211 Clone Distribution: clones will be
available through Research Genetics (www.resgen.com) The following
repetitive elements were found in this cDNA sequence: 1-28,
>AT_rich#Low_complexity 81-112, >AT_rich#Low_complexity
Seq primer: M13 Forward
POLYA=Yes.
FEATURES
            Location/Qualifiers
                1..515
                /organism="Sus scrofa"
                /strain="Crossbred"
                /db_xref="taxon:9823"
                /clone="MI-P-03-aba-f-02-1-0W"
                /clone_lib="MI-P-03"
                /lab_host="DH10B (Life Technologies)"
                /note="Vector: pT73D-pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: EcoRI. The MI-P-03

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